

SEQUENCE LISTING

(1) GENERAL INFORMATION:

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(ii) TITLE OF INVENTION: KERATINOCTYE GROWTH FACTOR-2

(iii) NUMBER OF SEQUENCES: 148

(iv) CORRESPONDENCE ADDRESS:

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(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 09/023,082
(B) FILING DATE: 13-FEB-1998
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: PCT/US95/01790
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(viii) PRIOR APPLICATION DATA:

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(B) FILING DATE: 05-JUN-1995

(ix) PRIOR APPLICATION DATA:

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(B) FILING DATE: 13-AUG-1996

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(B) FILING DATE: 28-FEB-1997

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: US 08/862,432
- (B) FILING DATE: 23-MAY-1997

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: US 08/910,875
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- (A) APPLICATION NUMBER: US 60/055,561
- (B) FILING DATE: 13-AUG-1997

(viii) ATTORNEY/AGENT INFORMATION:

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- (C) REFERENCE/DOCKET NUMBER: 1488.0360008/EKS

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: 202-371-2600
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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 627 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..624

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATG TGG AAA TGG ATA CTG ACA CAT TGT GCC TCA GCC TTT CCC CAC CTG	48
Met Trp Lys Trp Ile Leu Thr His Cys Ala Ser Ala Phe Pro His Leu	
1 5 10 15	
CCC GGC TGC TGC TGC TGC TTT TTG TTG CTG TTC TTG GTG TCT TCC	96
Pro Gly Cys Cys Cys Cys Phe Leu Leu Leu Phe Leu Val Ser Ser	
20 25 30	
GTC CCT GTC ACC TGC CAA GCC CTT GGT CAG GAC ATG GTG TCA CCA GAG	144
Val Pro Val Thr Cys Gln Ala Leu Gly Gln Asp Met Val Ser Pro Glu	
35 40 45	
GCC ACC AAC TCT TCT TCC TCC TTC TCC TCT CCT TCC AGC GCG GGA	192
Ala Thr Asn Ser Ser Ser Ser Phe Ser Ser Pro Ser Ser Ala Gly	
50 55 60	

AGG CAT GTG CCG AGC TAC AAT CAC CTT CAA GGA GAT GTC CGC TGG AGA Arg His Val Arg Ser Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg 65 70 75 80	240
AAG CTA TTC TCT TTC ACC AAG TAC TTT CTC AAG ATT GAG AAG AAC GGG Lys Leu Phe Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly 85 90 95	288
AAG GTC AGC GGG ACC AAG AAG GAG AAC TGC CCG TAC AGC ATC CTG GAG Lys Val Ser Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu 100 105 110	336
ATA ACA TCA GTA GAA ATC GGA GTT GTT GCC GTC AAA GCC ATT AAC AGC Ile Thr Ser Val Glu Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser 115 120 125	384
AAC TAT TAC TTA GCC ATG AAC AAG AAG GGG AAA CTC TAT GGC TCA AAA Asn Tyr Tyr Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys 130 135 140	432
GAA TTT AAC AAT GAC TGT AAG CTG AAG GAG AGG ATA GAG GAA AAT GGA Glu Phe Asn Asn Asp Cys Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly 145 150 155 160	480
TAC AAT ACC TAT GCA TCA TTT AAC TGG CAG CAT AAT GGG AGG CAA ATG Tyr Asn Thr Tyr Ala Ser Phe Asn Trp Gln His Asn Gly Arg Gln Met 165 170 175	528
TAT GTG GCA TTG AAT GGA AAA GGA GCT CCA AGG AGA GGA CAG AAA ACA Tyr Val Ala Leu Asn Gly Lys Gly Ala Pro Arg Arg Gly Gln Lys Thr 180 185 190	576
CGA AGG AAA AAC ACC TCT GCT CAC TTT CTT CCA ATG GTG GTA CAC TCA Arg Arg Lys Asn Thr Ser Ala His Phe Leu Pro Met Val Val His Ser 195 200 205	624
TAG	627

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Trp Lys Trp Ile Leu Thr His Cys Ala Ser Ala Phe Pro His Leu
1 5 10 15

Pro Gly Cys Cys Cys Cys Cys Phe Leu Leu Leu Phe Leu Val Ser Ser
20 25 30

Val Pro Val Thr Cys Gln Ala Leu Gly Gln Asp Met Val Ser Pro Glu
35 40 45

Ala Thr Asn Ser Ser Ser Ser Phe Ser Ser Pro Ser Ser Ala Gly
50 55 60

Arg His Val Arg Ser Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg
65 70 75 80

Lys Leu Phe Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly
85 90 95

Lys Val Ser Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu
100 105 110

Ile Thr Ser Val Glu Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser
115 120 125

Asn Tyr Tyr Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys
130 135 140

Glu Phe Asn Asn Asp Cys Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly
145 150 155 160

Tyr Asn Thr Tyr Ala Ser Phe Asn Trp Gln His Asn Gly Arg Gln Met
165 170 175

Tyr Val Ala Leu Asn Gly Lys Gly Ala Pro Arg Arg Gly Gln Lys Thr
180 185 190

Arg Arg Lys Asn Thr Ser Ala His Phe Leu Pro Met Val Val His Ser
195 200 205

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CCCCACATGT GGAAATGGAT ACTGACACAT TGTGCC

36

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CCCAAGCTTC CACAAACGTT GCCTTCCTCT ATGAG

35

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CATGCCATGG CGTGCCAAGC CCTTGGTCAG GACATG

36

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CCCAAGCTTC CACAAACGTT GCCTTCCTCT ATGAG

35

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GCGGGATCCG CCATCATGTG GAAATGGATA CTCAC

35

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GCGCGGTACC ACAAACGTTG CCTTCCT

27

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TAACGAGGAT CCGCCATCAT GTGGAAATGG ATACTGACAC

40

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TAAGCACTCG AGTGAGTGTA CCACCATTGG AAGAAAATG

38

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATTAACCCTC ACTAAAGGGA GGCCATGTGG AAATGGATAC TGACACATTG TGCC

54

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CCCAAGCTTC CACAAACGTT GCCTTCCTCT ATGAG

35

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 206 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met Ser Gly Pro Gly Thr Ala Ala Val Ala Leu Leu Pro Ala Val Leu
1 5 10 15

Leu Ala Leu Leu Ala Pro Trp Ala Gly Arg Gly Gly Ala Ala Ala Pro
20 25 30

Thr Ala Pro Asn Gly Thr Leu Glu Ala Glu Leu Glu Arg Arg Trp Glu
35 40 45

Ser Leu Val Ala Leu Ser Leu Ala Arg Leu Pro Val Ala Ala Gln Pro
50 55 60

Lys Glu Ala Ala Val Gln Ser Gly Ala Gly Asp Tyr Leu Leu Gly Ile
65 70 75 80

Lys Arg Leu Arg Arg Leu Tyr Cys Asn Val Gly Ile Gly Phe His Leu
85 90 95

Gln Ala Leu Pro Asp Gly Arg Ile Gly Gly Ala His Ala Asp Thr Arg
100 105 110

Asp Ser Leu Leu Glu Leu Ser Pro Val Glu Arg Gly Val Val Ser Ile
115 120 125

Phe Gly Val Ala Ser Arg Phe Phe Val Ala Met Ser Ser Lys Gly Lys
130 135 140

Leu Tyr Gly Ser Pro Phe Phe Thr Asp Glu Cys Thr Phe Lys Glu Ile
145 150 155 160

Leu Leu Pro Asn Asn Tyr Asn Ala Tyr Glu Ser Tyr Lys Tyr Pro Gly
165 170 175

Met Phe Ile Ala Leu Ser Lys Asn Gly Lys Thr Lys Lys Gly Asn Arg
180 185 190

Val Ser Pro Thr Met Lys Val Thr His Phe Leu Pro Arg Leu
195 200 205

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met Ser Arg Gly Ala Gly Arg Leu Gln Gly Thr Leu Trp Ala Leu Val
1 5 10 15

Phe Leu Gly Ile Leu Val Gly Met Val Val Pro Ser Pro Ala Gly Thr

20

25

30

Arg Ala Asn Asn Thr Leu Leu Asp Ser Arg Gly Trp Gly Thr Leu Leu
35 40 45

Ser Arg Ser Arg Ala Gly Leu Ala Gly Glu Ile Ala Gly Val Asn Trp
50 55 60

Glu Ser Gly Tyr Leu Val Gly Ile Lys Arg Gln Arg Arg Leu Tyr Cys
65 70 75 80

Asn Val Gly Ile Gly Phe His Leu Gln Val Leu Pro Asp Gly Arg Ile
85 90 95

Ser Gly Thr His Glu Glu Asn Pro Tyr Ser Leu Leu Glu Ile Ser Thr
100 105 110

Val Glu Arg Gly Val Val Ser Leu Phe Gly Val Arg Ser Ala Leu Phe
115 120 125

Val Ala Met Asn Ser Lys Gly Arg Leu Tyr Ala Thr Pro Ser Phe Gln
130 135 140

Glu Glu Cys Lys Phe Arg Glu Thr Leu Leu Pro Asn Asn Tyr Asn Ala
145 150 155 160

Tyr Glu Ser Asp Leu Tyr Gln Gly Thr Tyr Ile Ala Leu Ser Lys Tyr
165 170 175

Gly Arg Val Lys Arg Gly Ser Lys Val Ser Pro Ile Met Thr Val Thr
180 185 190

His Phe Leu Pro Arg Ile
195

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 268 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

• (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Met Ser Leu Ser Phe Leu Leu Leu Phe Phe Ser His Leu Ile Leu
1 5 10 15

Ser Ala Trp Ala His Gly Glu Lys Arg Leu Ala Pro Lys Gly Gln Pro
20 25 30

Gly Pro Ala Ala Thr Asp Arg Asn Pro Arg Gly Ser Ser Ser Arg Gln
35 40 45

Ser Ser Ser Ser Ala Met Ser Ser Ser Ala Ser Ser Ser Pro Ala
50 55 60

Ala Ser Leu Gly Ser Gln Gly Ser Gly Leu Glu Gln Ser Ser Phe Gln
65 70 75 80

Trp Ser Pro Ser Gly Arg Arg Thr Gly Ser Leu Tyr Cys Arg Val Gly
85 90 95

Ile Gly Phe His Leu Gln Ile Tyr Pro Asp Gly Lys Val Asn Gly Ser
100 105 110

His Glu Ala Asn Met Leu Ser Val Leu Glu Ile Phe Ala Val Ser Gln
115 120 125

Gly Ile Val Gly Ile Arg Gly Val Phe Ser Asn Lys Phe Leu Ala Met
130 135 140

Ser Lys Lys Gly Lys Leu His Ala Ser Ala Lys Phe Thr Asp Asp Cys
145 150 155 160

Lys Phe Arg Glu Arg Phe Gln Glu Asn Ser Tyr Asn Thr Tyr Ala Ser
165 170 175

Ala Ile His Arg Thr Glu Lys Thr Gly Arg Glu Trp Tyr Val Ala Leu
180 185 190

Asn Lys Arg Gly Lys Ala Lys Arg Gly Cys Ser Pro Arg Val Lys Pro
195 200 205

Gln His Ile Ser Thr His Phe Leu Pro Arg Phe Lys Gln Ser Glu Gln
210 215 220

Pro Glu Leu Ser Phe Thr Val Thr Val Pro Glu Lys Lys Asn Pro Pro
225 230 235 240

Ser Pro Ile Lys Ser Lys Ile Pro Leu Ser Ala Pro Arg Lys Asn Thr
245 250 255

Asn Ser Val Lys Tyr Arg Leu Lys Phe Arg Phe Gly
260 265

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Met Ala Glu Gly Glu Ile Thr Thr Phe Thr Ala Leu Thr Glu Lys Phe
1 5 10 15

Asn Leu Pro Pro Gly Asn Tyr Lys Lys Pro Lys Leu Leu Tyr Cys Ser
20 25 30

Asn Gly Gly His Phe Leu Arg Ile Leu Pro Asp Gly Thr Val Asp Gly
35 40 45

Thr Arg Asp Arg Ser Asp Gln His Ile Gln Leu Gln Leu Ser Ala Glu
50 55 60

Ser Val Gly Glu Val Tyr Ile Lys Ser Thr Glu Thr Gly Gln Tyr Leu
65 70 75 80

Ala Met Asp Thr Asp Gly Leu Leu Tyr Gly Ser Gln Thr Pro Asn Glu
85 90 95

Glu Cys Leu Phe Leu Glu Arg Leu Glu Glu Asn His Tyr Asn Thr Tyr
100 105 110

Ile Ser Lys Lys His Ala Glu Lys Asn Trp Phe Val Gly Leu Lys Lys
115 120 125

Asn Gly Ser Cys Lys Arg Gly Pro Arg Thr His Tyr Gly Gln Lys Ala
130 135 140

Ile Leu Phe Leu Pro Leu Pro Val Ser Ser Asp
145 150 155

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Met Ala Ala Gly Ser Ile Thr Thr Leu Pro Ala Leu Pro Glu Asp Gly
1 5 10 15

Gly Ser Gly Ala Phe Pro Pro Gly His Phe Lys Asp Pro Lys Arg Leu
20 25 30

Tyr Cys Lys Asn Gly Gly Phe Phe Leu Arg Ile His Pro Asp Gly Arg
35 40 45

Val Asp Gly Val Arg Glu Lys Ser Asp Pro His Ile Lys Leu Gln Leu
50 55 60

Gln Ala Glu Glu Arg Gly Val Val Ser Ile Lys Gly Val Cys Ala Asn
65 70 75 80

Arg Tyr Leu Ala Met Lys Glu Asp Gly Arg Leu Leu Ala Ser Lys Cys
85 90 95

Val Thr Asp Glu Cys Phe Phe Glu Arg Leu Glu Ser Asn Asn Tyr
100 105 110

Asn Thr Tyr Arg Ser Arg Lys Tyr Thr Ser Trp Tyr Val Ala Leu Lys
115 120 125

Arg Thr Gly Gln Tyr Lys Leu Gly Ser Lys Thr Gly Pro Gly Gln Lys
130 135 140

Ala Ile Leu Phe Leu Pro Met Ser Ala Lys Ser
145 150 155

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Met Ala Pro Leu Gly Glu Val Gly Asn Tyr Phe Gly Val Gln Asp Ala
1 5 10 15

Val Pro Phe Gly Asn Val Pro Val Leu Pro Val Asp Ser Pro Val Leu
20 25 30

Leu Ser Asp His Leu Gly Gln Ser Glu Ala Gly Gly Leu Pro Arg Gly
35 40 45

Pro Ala Val Thr Asp Leu Asp His Leu Lys Gly Ile Leu Arg Arg Arg
50 55 60

Gln Leu Tyr Cys Arg Thr Gly Phe His Leu Glu Ile Phe Pro Asn Gly
65 70 75 80

Thr Ile Gln Gly Thr Arg Lys Asp His Ser Arg Phe Gly Ile Leu Glu

85

90

95

Phe Ile Ser Ile Ala Val Gly Leu Val Ser Ile Arg Gly Val Asp Ser
100 105 110

Gly Leu Tyr Leu Gly Met Asn Glu Lys Gly Glu Leu Tyr Gly Ser Glu
115 120 125

Lys Leu Thr Gln Glu Cys Val Phe Arg Glu Gln Phe Glu Glu Asn Trp
130 135 140

Tyr Asn Thr Tyr Ser Ser Asn Leu Tyr Lys His Val Asp Thr Gly Arg
145 150 155 160

Arg Tyr Tyr Val Ala Leu Asn Lys Asp Gly Thr Pro Arg Glu Gly Thr
165 170 175

Arg Thr Lys Arg His Gln Lys Phe Thr His Phe Leu Pro Arg Pro Val
180 185 190

Asp Pro Asp Lys Val Pro Glu Leu Tyr Lys Asp Ile Leu Ser Gln Ser
195 200 205

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 194 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Met His Lys Trp Ile Leu Thr Trp Ile Leu Pro Thr Leu Leu Tyr Arg
1 5 10 15

Ser Cys Phe His Ile Ile Cys Leu Val Gly Thr Ile Ser Leu Ala Cys
20 25 30

Asn Asp Met Thr Pro Glu Gln Met Ala Thr Asn Val Asn Cys Ser Ser
35 40 45

Pro Glu Arg His Thr Arg Ser Tyr Asp Tyr Met Glu Gly Gly Asp Ile
50 55 60

Arg Val Arg Arg Leu Phe Cys Arg Thr Gln Trp Tyr Leu Arg Ile Asp
65 70 75 80

Lys Arg Gly Lys Val Lys Gly Thr Gln Glu Met Lys Asn Asn Tyr Asn

85

90

95

Ile Met Glu Ile Arg Thr Val Ala Val Gly Ile Val Ala Ile Lys Gly
100 105 110

Val Glu Ser Glu Phe Tyr Leu Ala Met Asn Lys Glu Gly Lys Leu Tyr
115 120 125

Ala Lys Lys Glu Cys Asn Glu Asp Cys Asn Phe Lys Glu Leu Ile Leu
130 135 140

Glu Asn His Tyr Asn Thr Tyr Ala Ser Ala Lys Trp Thr His Asn Gly
145 150 155 160

Gly Glu Met Phe Val Ala Leu Asn Gln Lys Gly Ile Pro Val Arg Gly
165 170 175

Lys Lys Thr Lys Lys Glu Gln Lys Thr Ala His Phe Leu Pro Met Ala
180 185 190

Ile Thr

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Met Trp Lys Trp Ile Leu Thr His Cys Ala Ser Ala Phe Pro His Leu
1 5 10 15

Pro Gly Cys Cys Cys Cys Phe Leu Leu Leu Phe Leu Val Ser Ser
20 25 30

Val Pro Val Thr Cys Gln Ala Leu Gly Gln Asp Met Val Ser Pro Glu
35 40 45

Ala Thr Asn Ser Ser Ser Ser Phe Ser Ser Pro Ser Ser Ala Gly
50 55 60

Arg His Val Arg Ser Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg
65 70 75 80

Lys Leu Phe Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly
85 90 95

Lys Val Ser Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu
100 105 110

Ile Thr Ser Val Glu Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser
115 120 125

Asn Tyr Tyr Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys
130 135 140

Glu Phe Asn Asn Asp Cys Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly
145 150 155 160

Tyr Asn Thr Tyr Ala Ser Phe Asn Trp Gln His Asn Gly Arg Gln Met
165 170 175

Tyr Val Ala Leu Asn Gly Lys Gly Ala Pro Arg Arg Gly Gln Lys Thr
180 185 190

Arg Arg Lys Asn Thr Ser Ala His Phe Leu Pro Met Val Val His Ser
195 200 205

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 239 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Met Gly Leu Ile Trp Leu Leu Leu Ser Leu Leu Glu Pro Gly Trp
1 5 10 15

Pro Ala Ala Gly Pro Gly Ala Arg Leu Arg Arg Asp Ala Gly Gly Arg
20 25 30

Gly Gly Val Tyr Glu His Leu Gly Gly Ala Pro Arg Arg Arg Lys Leu
35 40 45

Tyr Cys Ala Thr Lys Tyr His Leu Gln Leu His Pro Ser Gly Arg Val
50 55 60

Asn Gly Ser Leu Glu Asn Ser Ala Tyr Ser Ile Leu Glu Ile Thr Ala
65 70 75 80

Val Glu Val Gly Ile Val Ala Ile Arg Gly Leu Phe Ser Gly Arg Tyr
85 90 95

Leu Ala Met Asn Lys Arg Gly Arg Leu Tyr Ala Ser Glu His Tyr Ser
100 105 110

Ala Glu Cys Glu Phe Val Glu Arg Ile His Glu Leu Gly Tyr Asn Thr
115 120 125

Tyr Ala Ser Arg Leu Tyr Arg Thr Val Ser Ser Thr Pro Gly Ala Arg
130 135 140

Arg Gln Pro Ser Ala Glu Arg Leu Trp Tyr Val Ser Val Asn Gly Lys
145 150 155 160

Gly Arg Pro Arg Arg Gly Phe Lys Thr Arg Arg Thr Gln Lys Ser Ser
165 170 175

Leu Phe Leu Pro Arg Val Leu Asp His Arg Asp His Glu Met Val Arg
180 185 190

Gln Leu Gln Ser Gly Leu Pro Arg Pro Pro Gly Lys Gly Val Gln Pro
195 200 205

Arg Arg Arg Arg Gln Lys Gln Ser Pro Asp Asn Leu Glu Pro Ser His
210 215 220

Val Gln Ala Ser Arg Leu Gly Ser Gln Leu Glu Ala Ser Ala His
225 230 235

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 268 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Met Gly Ser Pro Arg Ser Ala Leu Ser Cys Leu Leu Leu His Leu Leu
1 5 10 15

Val Leu Cys Leu Gln Ala Gln Val Arg Ser Ala Ala Gln Lys Arg Gly
20 25 30

Pro Gly Ala Gly Asn Pro Ala Asp Thr Leu Gly Gln Gly His Glu Asp
35 40 45

Arg Pro Phe Gly Gln Arg Ser Arg Ala Gly Lys Asn Phe Thr Asn Pro
50 55 60

Ala Pro Asn Tyr Pro Glu Glu Gly Ser Lys Glu Gln Arg Asp Ser Val

65	70	75	80
Leu Pro Lys Val Thr Gln Arg His Val Arg Glu Gln Ser Leu Val Thr			
85		90	95
Asp Gln Leu Ser Arg Arg Leu Ile Arg Thr Tyr Gln Leu Tyr Ser Arg			
100		105	110
Thr Ser Gly Lys His Val Gln Val Leu Ala Asn Lys Arg Ile Asn Ala			
115		120	125
Met Ala Glu Asp Gly Asp Pro Phe Ala Lys Leu Ile Val Glu Thr Asp			
130		135	140
Thr Phe Gly Ser Arg Val Arg Val Arg Gly Ala Glu Thr Gly Leu Tyr			
145.	150	155	160
Ile Cys Met Asn Lys Lys Gly Lys Leu Ile Ala Lys Ser Asn Gly Lys			
165		170	175
Gly Lys Asp Cys Val Phe Thr Glu Ile Val Leu Glu Asn Asn Tyr Thr			
180		185	190
Ala Leu Gln Asn Ala Lys Tyr Glu Gly Trp Tyr Met Ala Phe Thr Arg			
195		200	205
Lys Gly Arg Pro Arg Lys Gly Ser Lys Thr Arg Gln His Gln Arg Glu			
210		215	220
Val His Phe Met Lys Arg Leu Pro Arg Gly His His Thr Thr Glu Gln			
225		230	235
Ser Leu Arg Phe Glu Phe Leu Asn Tyr Pro Pro Phe Thr Arg Ser Leu			
245		250	255
Arg Gly Ser Gln Arg Thr Trp Ala Pro Glu Pro Arg			
260		265	

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 593..1216

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GGAATTCCGG	GAAGAGAGGG	AAGAAAACAA	CGGCGACTGG	GCAGCTGCCT	CCACTTCTGA	60
CAACTCCAAA	GGGATATACT	TGTAGAAGTG	GCTCGCAGGC	TGGGGCTCCG	CAGAGAGAGA	120
CCAGAAGGTG	CCAACCGCAG	AGGGGTGCAG	ATATCTCCCC	CTATTCCCCA	CCCCACCTCC	180
CTTGGGTTTT	GTTCAACCGTG	CTGTCATCTG	TTTTTCAGAC	CTTTTTGGCA	TCTAACATGG	240
TGAAGAAAGG	AGTAAAGAAG	AGAACAAAGT	AACTCCTGGG	GGAGCGAAGA	GCGCTGGTGA	300
CCAACACCAAC	CAACGCCACC	ACCAGCTCCT	GCTGCTGCAG	CCACCCACGT	CCACCATTAA	360
CCGGGAGGCT	CCAGAGGCAGT	AGGCAGCGGA	TCCGAGAAAG	GAGCGAGGGG	AGTCAGCCGG	420
CTTTTCCGAG	GAGTTATGGA	TGTTGGTGCA	TTCACTTCTG	GCCAGATCCG	CGCCCCAGAGG	480
GAGCTAACCA	GCAGCCACCA	CCTCGAGCTC	TCTCCTTGCC	TTGCATCGGG	TCTTACCCCTT	540
CCAGTATGTT	CCTTCTGATG	AGACAATTTC	CAGTGCCGAG	AGTTTCAGTA	CA ATG	595
				Met		
				1		
TGG AAA TGG ATA CTG ACA CAT TGT	GCC TCA	GCC TTT CCC	CAC CTG CCC			643
Trp Lys Trp Ile Leu Thr His Cys	Ala Ser Ala	Phe Pro His	Leu Pro			
5	10	15				
GGC TGC TGC TGC TGC TTT TTG	CTG TTC TTG	GTG TCT TCC	GTC			691
Gly Cys Cys Cys Cys	Phe Leu Leu Leu	Phe Leu Val	Ser Ser Val			
20	25	30				
CCT GTC ACC TGC CAA GCC CTT GGT	CAG GAC ATG	GTG TCA CCA GAG	GCC			739
Pro Val Thr Cys Gln Ala Leu	Gly Gln Asp	Met Val Ser	Pro Glu Ala			
35	40	45				
ACC AAC TCT TCC TCC TTC	TCC TCT CCT	AGC GCG GGA AGG				787
Thr Asn Ser Ser Ser Ser	Phe Ser Ser Pro	Ser Ser Ala Gly Arg				
50	55	60	65			
CAT GTG CGG AGC TAC AAT CAC	CTT CAA GGA GAT	GTC CGC TGG AGA AAG				835
His Val Arg Ser Tyr Asn His	Leu Gln Gly Asp	Val Arg Trp Arg Lys				
70	75	80				
CTA TTC TCT ACC AAG TAC	TTT CTC AAG ATT	GAG AAG AAC GGG AAG				883
Leu Phe Ser Thr Lys Tyr Phe	Leu Lys Ile Glu Lys Asn	Gly Lys				
85	90	95				
GTC AGC GGG ACC AAG AAG	GAG AAC TGC CCG	TAC AGC ATC CTG GAG ATA				931
Val Ser Gly Thr Lys Lys	Glu Asn Cys Pro	Tyr Ser Ile Leu Glu Ile				
100	105	110				
ACA TCA GTA GAA ATC GGA	GTT GCC GTC AAA	GCC ATT AAC AGC AAC				979
Thr Ser Val Glu Ile Gly Val	Val Ala Val Lys	Ala Ile Asn Ser Asn				
115	120	125				
TAT TAC TTA GCC ATG AAC	AAG AAG GGG AAA	CTC TAT GGC TCA AAA GAA				1027

TTCTTGCCAA ATGTCATGGC GGTAAAGAGG CTGTCACAT CTCTAAAAAC CCTCTGTAAA	2356
TTCCACATAA TGCATCTTC CAAAGGAAC TATAAAGAAT TTGGTATGAA GCGCAACTCT	2416
CCCAGGGCT TAAACTGAGC AAATCAAATA TATACTGGTA TATGTGTAAC CATATACAAA	2476
AACCTGTTCT AGCTGTATGA TCTAGTCTT ACAAAACCAA ATAAAACCTG TTTTCTGTAA	2536
ATTAAAGAG CTTTACAAGG TTCCATAATG TAACCATATC AAAATTCAATT TTGTTAGAGC	2596
ACGTATAGAA AAGAGTACAT AAGAGTTAC CAATCATCAT CACATTGTAT TCCACTAAAT	2656
AAATACATAA GCCTTATTTG CAGTGTCTGT AGTGATTTA AAAATGTAGA AAAATACTAT	2716
TTGTTCTAAA TACTTTAAG CAATAACTAT AATAGTATAT TGATGCTGCA GTTTTATCTT	2776
CATATTTCTT GTTTGAAAA AGCATTATG TGTTGGACA CAGTATTTG GTACAAAAAA	2836
AAAGACTCAC TAAATGTGTC TTACTAAAGT TTAAACCTTG GAAATGCTGG CGTTCTGTGA	2896
TTCTCCAACA AACTTATTTG TGTCAAAACT TAACCAGCAC TTCCAGTTAA TCTGTTATTT	2956
TTAAAAATTG CTTTATTAAG AAATTTTG TATAATCCC TAAAAGGTCA TATTTTCCC	3016
ATTCTTCAAA AAAACTGTAT TTCAGAAGAA ACACATTGA GGCAGTGTCT TTTGGCTTAT	3076
AGTTTAAATT GCATTTCATC ATACTTGCT TCCAACCTGC TTTTGGCAA ATGAGATTAT	3136
AAAAATGTTT AATTTTGTTG GTTGGAAATCT GGATGTTAAA ATTTAATTGG TAACTCAGTC	3196
TGTGAGCTAT AATGTAATGC ATTCCTATCC AAACATAGGTAA TCTTTTTTC CTTTATGTTG	3256
AAATAATAAT GGCACCTGAC ACATAGACAT AGACCACCCA CAACCTAAAT TAAATGTTG	3316
GTAAGACAAA TACACATTGG ATGACCACAG TAACAGCAAA CAGGGCACAA ACTGGATTCT	3376
TATTCACAT AGACATTTAG ATTACTAAAG AGGGCTATGT GTAAACAGTC ATCATTATAG	3436
TACTCAAGAC ACTAAAACAG CTTCTAGCCA AATATATTAA AGCTTGAGA GGCCAAAAAT	3496
AGAAAACATC TCCCCGTCT CTCACACATT TCCCTCACAG AAAGACAAAA AACCTGCCTG	3556
GTGCAGTAGC TCACACCTGT AATCCCAGCA GTTGGGAGA CTGTGGGAAG ATGGCTTGAG	3616
TCCAGGAGTT CTAGACAGGC CTGAGAAACC TAGTGAGACA TCCTTCTCTT AAACAAAACA	3676
AAACAAAACA AATGTAGCCA TGCAGGGTGG CATATACCTG TGGTCCAAAC TACTCAGGAG	3736
GCTGAAACGG AAGGATCTCT TGGGCCAG GAGTTGAGG CTGCAGTGAG CTATAATCTT	3796
GCCATTGCAC TCCAGCCTGG GTGAAAAGA GCCAGAAAGA AAGGAAAGAG AGAAAAGAGA	3856
AAAGAAAGAG AGAAAAGACA GAAAGACAGG AAGGAAGGAA GGAAGGAAGG AAGGAAGGAA	3916
GGAAGCAAGG AAAGAAGGAA GGAAGGAAAG AAGGGAGGGA AGGAAGGAGA GAGAAAGAAA	3976

GATTGTTGG	TAAGGAGTAA	TGACATTCTC	TTGCATTTAA	AAGTGGCATA	TTTGCTTGAA	4036
ATGGAAATAG	AATTCTGGTC	CCTTTGCAA	CTACTGAAGA	AAAAAAAAG	CAGTTTCAGC	4096
CCTGAATGTT	GTAGATTGAA	AAAAAAAAAA	AAAAAAACTC	GAGGGGGGGC	CCGTACCCAA	4156
TTCGCCCTAT	AGTGAGTCGT	A				4177

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Met	Trp	Lys	Trp	Ile	Leu	Thr	His	Cys	Ala	Ser	Ala	Phe	Pro	His	Leu
1				5					10					15	
Pro	Gly	Cys	Cys	Cys	Cys	Cys	Phe	Leu	Leu	Leu	Phe	Leu	Val	Ser	Ser
								20		25			30		
Val	Pro	Val	Thr	Cys	Gln	Ala	Leu	Gly	Gln	Asp	Met	Val	Ser	Pro	Glu
					35			40			45				
Ala	Thr	Asn	Ser	Ser	Ser	Ser	Phe	Ser	Ser	Pro	Ser	Ser	Ala	Gly	
		50			55				60						
Arg	His	Val	Arg	Ser	Tyr	Asn	His	Leu	Gln	Gly	Asp	Val	Arg	Trp	Arg
		65			70				75			80			
Lys	Leu	Phe	Ser	Phe	Thr	Lys	Tyr	Phe	Leu	Lys	Ile	Glu	Lys	Asn	Gly
					85				90			95			
Lys	Val	Ser	Gly	Thr	Lys	Lys	Glu	Asn	Cys	Pro	Tyr	Ser	Ile	Leu	Glu
					100				105			110			
Ile	Thr	Ser	Val	Glu	Ile	Gly	Val	Val	Ala	Val	Lys	Ala	Ile	Asn	Ser
					115			120			125				
Asn	Tyr	Tyr	Leu	Ala	Met	Asn	Lys	Lys	Gly	Lys	Leu	Tyr	Gly	Ser	Lys
					130			135			140				
Glu	Phe	Asn	Asn	Asp	Cys	Lys	Leu	Lys	Glu	Arg	Ile	Glu	Glu	Asn	Gly
					145			150			155			160	
Tyr	Asn	Thr	Tyr	Ala	Ser	Phe	Asn	Trp	Gln	His	Asn	Gly	Arg	Gln	Met
					165				170			175			
Tyr	Val	Ala	Leu	Asn	Gly	Lys	Gly	Ala	Pro	Arg	Arg	Gly	Gln	Lys	Thr
					180			185			190				

Arg Arg Lys Asn Thr Ser Ala His Phe Leu Pro Met Val Val His Ser
195 200 205

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Gly Gln Asp Met Val Ser Pro Glu Ala Thr Asn Ser Ser Ser Ser Ser
1 5 10 15

Phe Ser Ser Pro Ser Ser Ala Gly Arg His Val Arg Ser Tyr Asn
20 25 30

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Lys Ile Glu Lys Asn Gly Lys Val Ser Gly Thr Lys Lys Glu Asn Cys
1 5 10 15

Pro Tyr Ser

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Asn	Lys	Lys	Gly	Lys	Leu	Tyr	Gly	Ser	Lys	Glu	Phe	Asn	Asn	Asp	Cys
1					5				10					15	
Lys	Leu	Lys	Glu	Arg	Ile	Glu	Glu	Asn	Gly	Tyr	Asn	Thr	Tyr		
					20				25					30	

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Asn	Gly	Lys	Gly	Ala	Pro	Arg	Arg	Gly	Gln	Lys	Thr	Arg	Arg	Lys	Asn
1					5					10				15	
Thr	Ser	Ala													

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 555 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..553

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

ATG	AGA	GGA	TCG	CAT	CAC	CAT	CAC	CAT	CAC	GGA	TCC	TGC	CAG	GCT	CTG
Met	Arg	Gly	Ser	His	His	His	His	His	His	Gly	Ser	Cys	Gln	Ala	Leu
1				5						10				15	

GGT CAG GAC ATG GTT TCT CCG GAA GCT ACC AAC TCT TCC TCT TCC TCT Gly Gln Asp Met Val Ser Pro Glu Ala Thr Asn Ser Ser Ser Ser Ser	96
20 25 30	
TTC TCT TCC CCG TCT TCC GCT GGT CGT CAC GTT CGT TCT TAC AAC CAC Phe Ser Ser Pro Ser Ser Ala Gly Arg His Val Arg Ser Tyr Asn His	144
35 40 45	
CTG CAG GGT GAC GTT CGT TGG CGT AAA CTG TTC TCT TTC ACC AAA TAC Leu Gln Gly Asp Val Arg Trp Arg Lys Leu Phe Ser Phe Thr Lys Tyr	192
50 55 60	
TTC CTG AAA ATC GAA AAA AAC GGT AAA GTT TCT GGG ACC AAG AAG GAG Phe Leu Lys Ile Glu Lys Asn Gly Lys Val Ser Gly Thr Lys Lys Glu	240
65 70 75 80	
AAC TGC CCG TAC AGC ATC CTG GAG ATA ACA TCA GTA GAA ATC GGA GTT Asn Cys Pro Tyr Ser Ile Leu Glu Ile Thr Ser Val Glu Ile Gly Val	288
85 90 95	
GTT GCC GTC AAA GCC ATT AAC AGC AAC TAT TAC TTA GCC ATG AAC AAG Val Ala Val Lys Ala Ile Asn Ser Asn Tyr Tyr Leu Ala Met Asn Lys	336
100 105 110	
AAG GGG AAA CTC TAT GGC TCA AAA GAA TTT AAC AAT GAC TGT AAG CTG Lys Gly Lys Leu Tyr Gly Ser Lys Glu Phe Asn Asn Asp Cys Lys Leu	384
115 120 125	
AAG GAG AGG ATA GAG GAA AAT GGA TAC AAT ACC TAT GCA TCA TTT AAC Lys Glu Arg Ile Glu Glu Asn Gly Tyr Asn Thr Tyr Ala Ser Phe Asn	432
130 135 140	
TGG CAG CAT AAT GGG AGG CAA ATG TAT GTG GCA TTG AAT GGA AAA GGA Trp Gln His Asn Gly Arg Gln Met Tyr Val Ala Leu Asn Gly Lys Gly	480
145 150 155 160	
GCT CCA AGG AGA GGA CAG AAA ACA CGA AGG AAA AAC ACC TCT GCT CAC Ala Pro Arg Arg Gly Gln Lys Thr Arg Arg Lys Asn Thr Ser Ala His	528
165 170 175	
TTT CTT CCA ATG GTG GTA CAC TCA TAG Phe Leu Pro Met Val Val His Ser	555
180	

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 184 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Met Arg Gly Ser His His His His His His Gly Ser Cys Gln Ala Leu
1 5 10 15

Gly Gln Asp Met Val Ser Pro Glu Ala Thr Asn Ser Ser Ser Ser Ser
20 25 30

Phe Ser Ser Pro Ser Ser Ala Gly Arg His Val Arg Ser Tyr Asn His
35 40 45

Leu Gln Gly Asp Val Arg Trp Arg Lys Leu Phe Ser Phe Thr Lys Tyr
50 55 60

Phe Leu Lys Ile Glu Lys Asn Gly Lys Val Ser Gly Thr Lys Lys Glu
65 70 75 80

Asn Cys Pro Tyr Ser Ile Leu Glu Ile Thr Ser Val Glu Ile Gly Val
85 90 95

Val Ala Val Lys Ala Ile Asn Ser Asn Tyr Tyr Leu Ala Met Asn Lys
100 105 110

Lys Gly Lys Leu Tyr Gly Ser Lys Glu Phe Asn Asn Asp Cys Lys Leu
115 120 125

Lys Glu Arg Ile Glu Glu Asn Gly Tyr Asn Thr Tyr Ala Ser Phe Asn
130 135 140

Trp Gln His Asn Gly Arg Gln Met Tyr Val Ala Leu Asn Gly Lys Gly
145 150 155 160

Ala Pro Arg Arg Gly Gln Lys Thr Arg Arg Lys Asn Thr Ser Ala His
165 170 175

Phe Leu Pro Met Val Val His Ser
180

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

ATGTGGAAAT GGATACTGAC CCACTGCGCT TCTGCTTCC CGCACCTGCC GGGTTGCTGC

60

TGCTGCTGCT TCCTGCTGCT GTTC

84

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CCGGAGAAC CATGTCCTGA CCCAGAGCCT GGCAGGTAAC CGGAACAGAA GAAACCAGGA

60

ACAGCAGCAG GAAGCAGCAG CA

82

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

GGGTCAGGAC ATGGTTTCTC CGGAAGCTAC CAACTCTTCT TCTTCTTCTT TCTCTTCTCC

60

GTCTTCTGCT GGTCGTCACG

80

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GGTGAAAGAG AACAGTTTAC GCCAACGAAC GTCACCCTGC AGGTGGTTGT AAGAACGAAC	60
GTGACGACCA GCAGAAGACG G	81

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

CGTTGGCGTA AACTGTTCTC TTTCACCAAA TACTTCCTGA AAATCGAAAA AAACGGTAAA	60
GTTTCTGGGA CCAAA	75

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

TTTGGTCCCA GAAACTTAC CGTTTTTC GATTTTCAG	39
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(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

AAAGGATCCA TGTGGAAATG GATACTGACC CACTGC

36

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 627 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..624

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

ATG TGG AAA TGG ATA CTG ACC CAC TGC GCT TCT GCT TTC CCG CAC CTG Met Trp Lys Trp Ile Leu Thr His Cys Ala Ser Ala Phe Pro His Leu	48
1 5 10 15	
CCG GGT TGC TGC TGC TGC TTC CTG CTG CTG TTC CTG GTT TCT TCT Pro Gly Cys Cys Cys Cys Phe Leu Leu Leu Phe Leu Val Ser Ser	96
20 25 30	
GTT CCG GTT ACC TGC CAG GCT CTG GGT CAG GAC ATG GTT TCT CCG GAA Val Pro Val Thr Cys Gln Ala Leu Gly Gln Asp Met Val Ser Pro Glu	144
35 40 45	
GCT ACC AAC TCT TCC TCT TCC TTC TCT TCC CCG ACT TCC GCT GGT Ala Thr Asn Ser Ser Ser Phe Ser Ser Pro Thr Ser Ala Gly	192
50 55 60	
CGT CAC GTT CGT TCT TAC AAC CAC CTG CAG GGT GAC GTT CGT TGG CGT Arg His Val Arg Ser Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg	240
65 70 75 80	
AAA CTG TTC TCT TTC ACC AAA TAC TTC CTG AAA ATC GAA AAA AAC GGT Lys Leu Phe Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly	288
85 90 95	
AAA GTT TCT GGG ACC AAG AAG GAG AAC TGC CCG TAC AGC ATC CTG GAG Lys Val Ser Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu	336
100 105 110	
ATA ACA TCA GTA GAA ATC GGA GTT GTT GCC GTC AAA GCC ATT AAC AGC Ile Thr Ser Val Glu Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser	384
115 120 125	
AAC TAT TAC TTA GCC ATG AAC AAG AAG GGG AAA CTC TAT GGC TCA AAA Asn Tyr Tyr Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys	432
130 135 140	

GAA TTT AAC AAT GAC TGT AAG CTG AAG GAG AGG ATA GAG GAA AAT GGA	480
Glu Phe Asn Asn Asp Cys Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly	
145 150 155 160	
TAC AAT ACC TAT GCA TCA TTT AAC TGG CAG CAT AAT GGG AGG CAA ATG	528
Tyr Asn Thr Tyr Ala Ser Phe Asn Trp Gln His Asn Gly Arg Gln Met	
165 170 175	
TAT GTG GCA TTG AAT GGA AAA GGA GCT CCA AGG AGA GGA CAG AAA ACA	576
Tyr Val Ala Leu Asn Gly Lys Gly Ala Pro Arg Arg Gly Gln Lys Thr	
180 185 190	
CGA AGG AAA AAC ACC TCT GCT CAC TTT CTT CCA ATG GTG GTA CAC TCA	624
Arg Arg Lys Asn Thr Ser Ala His Phe Leu Pro Met Val Val His Ser	
195 200 205	
TAG	627

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 amino acids
- (B) TYPE: amino acid
- (C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Met Trp Lys Trp Ile Leu Thr His Cys Ala Ser Ala Phe Pro His Leu	
1 5 10 15	
Pro Gly Cys Cys Cys Cys Cys Phe Leu Leu Leu Phe Leu Val Ser Ser	
20 25 30	
Val Pro Val Thr Cys Gln Ala Leu Gly Gln Asp Met Val Ser Pro Glu	
35 40 45	
Ala Thr Asn Ser Ser Ser Ser Phe Ser Ser Pro Thr Ser Ala Gly	
50 55 60	
Arg His Val Arg Ser Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg	
65 70 75 80	
Lys Leu Phe Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly	
85 90 95	
Lys Val Ser Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu	
100 105 110	
Ile Thr Ser Val Glu Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser	
115 120 125	
Asn Tyr Tyr Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys	

130	135	140													
Glu	Phe	Asn	Asn	Asp	Cys	Lys	Leu	Lys	Glu	Arg	Ile	Glu	Glu	Asn	Gly
145					150				155					160	
Tyr	Asn	Thr	Tyr	Ala	Ser	Phe	Asn	Trp	Gln	His	Asn	Gly	Arg	Gln	Met
	165					170							175		
Tyr	Val	Ala	Leu	Asn	Gly	Lys	Gly	Ala	Pro	Arg	Arg	Gly	Gln	Lys	Thr
	180					185							190		
Arg	Arg	Lys	Asn	Thr	Ser	Ala	His	Phe	Leu	Pro	Met	Val	Val	His	Ser
	195					200						205			

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

TTTCATGACT TGTCAAGCTC TGGGTCAAGA TATGGTTC

38

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

GCCCAAGCTT CCACAAACGT TGCCTTCC

28

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 525 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..522

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

ATG ACC TGC CAG GCT CTG GGT CAG GAC ATG GTT TCT CCG GAA GCT ACC	48
Met Thr Cys Gln Ala Leu Gly Gln Asp Met Val Ser Pro Glu Ala Thr	
1 5 10 15	
AAC TCT TCC TCT TCC TTC TCT TCC CCG TCT TCC GCT GGT CGT CAC	96
Asn Ser Ser Ser Ser Phe Ser Ser Pro Ser Ser Ala Gly Arg His	
20 25 30	
GTT CGT TCT TAC AAC CAC CTG CAG GGT GAC GTT CGT TGG CGT AAA CTG	144
Val Arg Ser Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg Lys Leu	
35 40 45	
TTC TCT TTC ACC AAA TAC TTC CTG AAA ATC GAA AAA AAC GGT AAA GTT	192
Phe Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly Lys Val	
50 55 60	
TCT GGG ACC AAG AAG GAG AAC TGC CCG TAC AGC ATC CTG GAG ATA ACA	240
Ser Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu Ile Thr	
65 70 75 80	
TCA GTA GAA ATC GGA GTT GTT GCC GTC AAA GCC ATT AAC AGC AAC TAT	288
Ser Val Glu Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser Asn Tyr	
85 90 95	
TAC TTA GCC ATG AAC AAG AAG GGG AAA CTC TAT GGC TCA AAA GAA TTT	336
Tyr Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys Glu Phe	
100 105 110	
AAC AAT GAC TGT AAG CTG AAG GAG AGG ATA GAG GAA AAT GGA TAC AAT	384
Asn Asn Asp Cys Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly Tyr Asn	
115 120 125	
ACC TAT GCA TCA TTT AAC TGG CAG CAT AAT GGG AGG CAA ATG TAT GTG	432
Thr Tyr Ala Ser Phe Asn Trp Gln His Asn Gly Arg Gln Met Tyr Val	
130 135 140	
GCA TTG AAT GGA AAA GGA GCT CCA AGG AGA GGA CAG AAA ACA CGA AGG	480
Ala Leu Asn Gly Lys Gly Ala Pro Arg Arg Gly Gln Lys Thr Arg Arg	
145 150 155 160	
AAA AAC ACC TCT GCT CAC TTT CTT CCA ATG GTG GTA CAC TCA	522

Lys Asn Thr Ser Ala His Phe Leu Pro Met Val Val His Ser
165 170

TAG 525

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

Met Thr Cys Gln Ala Leu Gly Gln Asp Met Val Ser Pro Glu Ala Thr
1 5 10 15

Asn Ser Ser Ser Ser Phe Ser Ser Pro Ser Ser Ala Gly Arg His
20 25 30

Val Arg Ser Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg Lys Leu
35 40 45

Phe Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly Lys Val
50 55 60

Ser Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu Ile Thr
65 70 75 80

Ser Val Glu Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser Asn Tyr
85 90 95

Tyr Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys Glu Phe
100 105 110

Asn Asn Asp Cys Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly Tyr Asn
115 120 125

Thr Tyr Ala Ser Phe Asn Trp Gln His Asn Gly Arg Gln Met Tyr Val
130 135 140

Ala Leu Asn Gly Lys Gly Ala Pro Arg Arg Gly Gln Lys Thr Arg Arg
145 150 155 160

Lys Asn Thr Ser Ala His Phe Leu Pro Met Val Val His Ser
165 170

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

TCAGTGAAATT CATTAAAGAG GAGAAATTAA TCATGACTTG CCAGG

45

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 48 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

TCATGACTTG CCAGGCAGT GGTCAAGACA TGGTTTCCCC GGAAGCTA

48

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 48 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

GCTTCAGCAG CCCATCTAGC GCAGGGTCGTC ACGTTCGCTC TTACAACC

48

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 48 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

GTTCGTTGGC GCAAACGTGTT CAGCTTTACC AAGTACTTCC TGAAAATC

48

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

TCGAAAAAAA CGGTAAAGTT TCTGGGAC

28

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

GATGGGCTGC TGAAGCTAGA GCTGGAGCTG TTGGTAGCTT CCGGGGAA

48

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

AACAGTTTGC GCCAACGAAC ATCACCCCTGT AAGTGGTTGT AAGAG

45

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

TTCTTGGTCC CAGAAACTTT ACCGTTTTT TCGATTTCA GGAAGTA

47

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

TTCTTGGTCC CAGAAACTTT ACCG

24

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

AGATCAGGCT TCTATTATTA TGAGTGTACC ACCATTGGAA GAAAG

45

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 525 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..522

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

ATG ACT TGC CAG GCA CTG GGT CAA GAC ATG GTT TCC CCG GAA GCT ACC	48
Met Thr Cys Gln Ala Leu Gly Gln Asp Met Val Ser Pro Glu Ala Thr	
1 5 10 15	
AAC AGC TCC AGC TCT AGC TTC AGC AGC CCA TCT AGC GCA GGT CGT CAC	96
Asn Ser Ser Ser Ser Phe Ser Ser Pro Ser Ser Ala Gly Arg His	
20 25 30	
GTT CGC TCT TAC AAC CAC TTA CAG GGT GAT GTT CGT TGG CGC AAA CTG	144
Val Arg Ser Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg Lys Leu	
35 40 45	
TTC AGC TTT ACC AAG TAC TTC CTG AAA ATC GAA AAA AAC GGT AAA GTT	192
Phe Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly Lys Val	
50 55 60	
TCT GGG ACC AAG AAG GAG AAC TGC CCG TAC AGC ATC CTG GAG ATA ACA	240
Ser Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu Ile Thr	
65 70 75 80	
TCA GTA GAA ATC GGA GTT GTT GCC GTC AAA GCC ATT AAC AGC AAC TAT	288
Ser Val Glu Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser Asn Tyr	
85 90 95	
TAC TTA GCC ATG AAC AAG AAG GGG AAA CTC TAT GGC TCA AAA GAA TTT	336
Tyr Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys Glu Phe	
100 105 110	
AAC AAT GAC TGT AAG CTG AAG GAG AGG ATA GAG GAA AAT GGA TAC AAT	384
Asn Asn Asp Cys Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly Tyr Asn	
115 120 125	
ACC TAT GCA TCA TTT AAC TGG CAG CAT AAT GGG AGG CAA ATG TAT GTG	432
Thr Tyr Ala Ser Phe Asn Trp Gln His Asn Gly Arg Gln Met Tyr Val	
130 135 140	
GCA TTG AAT GGA AAA GGA GCT CCA AGG AGA GGA CAG AAA ACA CGA AGG	480

Ala	Leu	Asn	Gly	Lys	Gly	Ala	Pro	Arg	Arg	Gly	Gln	Lys	Thr	Arg	Arg
145						150					155				160
AAA	AAC	ACC	TCT	GCT	CAC	TTT	CTT	CCA	ATG	GTG	GTA	CAC	TCA		522
Lys	Asn	Thr	Ser	Ala	His	Phe	Leu	Pro	Met	Val	Val	His	Ser		
						165					170				
TAG															525

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Met	Thr	Cys	Gln	Ala	Leu	Gly	Gln	Asp	Met	Val	Ser	Pro	Glu	Ala	Thr
1					5					10					15
Asn	Ser	Ser	Ser	Ser	Ser	Phe	Ser	Ser	Pro	Ser	Ser	Ala	Gly	Arg	His
										25					30
Val	Arg	Ser	Tyr	Asn	His	Leu	Gln	Gly	Asp	Val	Arg	Trp	Arg	Lys	Leu
						35			40			45			
Phe	Ser	Phe	Thr	Lys	Tyr	Phe	Leu	Lys	Ile	Glu	Lys	Asn	Gly	Lys	Val
						50			55			60			
Ser	Gly	Thr	Lys	Lys	Glu	Asn	Cys	Pro	Tyr	Ser	Ile	Leu	Glu	Ile	Thr
						65			70			75			80
Ser	Val	Glu	Ile	Gly	Val	Val	Ala	Val	Lys	Ala	Ile	Asn	Ser	Asn	Tyr
						85			90			95			
Tyr	Leu	Ala	Met	Asn	Lys	Lys	Gly	Lys	Leu	Tyr	Gly	Ser	Lys	Glu	Phe
							100		105			110			
Asn	Asn	Asp	Cys	Lys	Leu	Lys	Glu	Arg	Ile	Glu	Glu	Asn	Gly	Tyr	Asn
						115			120			125			
Thr	Tyr	Ala	Ser	Phe	Asn	Trp	Gln	His	Asn	Gly	Arg	Gln	Met	Tyr	Val
						130			135			140			
Ala	Leu	Asn	Gly	Lys	Gly	Ala	Pro	Arg	Arg	Gly	Gln	Lys	Thr	Arg	Arg
145						150					155				160
Lys	Asn	Thr	Ser	Ala	His	Phe	Leu	Pro	Met	Val	Val	His	Ser		
						165					170				

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

GGACCCTCAT GACCTGCCAG GCTCTGGGTC AGGAC

35

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

GGACAGCCAT GGCTGGTCGT CACGTTCG

28

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

GGACAGCCAT GGTCGTTGG CGTAAACTG

29

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

GGACAGCCAT GGAAAAAAAC GGTAAAGTTT C

31

(2) INFORMATION FOR SEQ ID NO:60:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

GGACCCCCAT GGAGAACTGC CCGTAGAGC

29

(2) INFORMATION FOR SEQ ID NO:61:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

GGACCCCCAT GGTCAAAGCC ATTAACAGCA AC

32

(2) INFORMATION FOR SEQ ID NO:62:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

GGACCCCCAT GGGGAAACTC TATGGCTCAA AAG

33

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

CTGCCCAAGC TTATTATGAG TGTACCACCA TTGGAAG

37

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

CTGCCCAAGC TTATTACTTC AGCTTACAGT CATTGT

36

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 525 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 1..522

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

ATG ACC TGC CAG GCT CTG GGT CAG GAC ATG GTT TCT CCG GAA GCT ACC Met Thr Cys Gln Ala Leu Gly Gln Asp Met Val Ser Pro Glu Ala Thr	48
1 5 10 15	
AAC TCT TCC TCT TCC TTC TCT TCC CCG TCT TCC GCT GGT CGT CAC Asn Ser Ser Ser Ser Phe Ser Ser Pro Ser Ser Ala Gly Arg His	96
20 25 30	
GTT CGT TCT TAC AAC CAC CTG CAG GGT GAC GTT CGT TGG CGT AAA CTG Val Arg Ser Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg Lys Leu	144
35 40 45	
TTC TCT TTC ACC AAA TAC TTC CTG AAA ATC GAA AAA AAC GGT AAA GTT Phe Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly Lys Val	192
50 55 60	
TCT GGG ACC AAG AAG GAG AAC TGC CCG TAC AGC ATC CTG GAG ATA ACA Ser Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu Ile Thr	240
65 70 75 80	
TCA GTA GAA ATC GGA GTT GTT GCC GTC AAA GCC ATT AAC AGC AAC TAT Ser Val Glu Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser Asn Tyr	288
85 90 95	
TAC TTA GCC ATG AAC AAG AAG GGG AAA CTC TAT GGC TCA AAA GAA TTT Tyr Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys Glu Phe	336
100 105 110	
AAC AAT GAC TGT AAG CTG AAG GAG AGG ATA GAG GAA AAT GGA TAC AAT Asn Asn Asp Cys Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly Tyr Asn	384
115 120 125	
ACC TAT GCA TCA TTT AAC TGG CAG CAT AAT GGG AGG CAA ATG TAT GTG Thr Tyr Ala Ser Phe Asn Trp Gln His Asn Gly Arg Gln Met Tyr Val	432
130 135 140	
GCA TTG AAT GGA AAA GGA GCT CCA AGG AGA GGA CAG AAA ACA CGA AGG Ala Leu Asn Gly Lys Gly Ala Pro Arg Arg Gly Gln Lys Thr Arg Arg	480
145 150 155 160	
AAA AAC ACC TCT GCT CAC TTT CCA ATG GTG GTA CAC TCA Lys Asn Thr Ser Ala His Phe Leu Pro Met Val Val His Ser	522
165 170	
TAG	525

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids
- (B) TYPE: amino acid
- (C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

Met Thr Cys Gln Ala Leu Gly Gln Asp Met Val Ser Pro Glu Ala Thr
1 5 10 15

Asn Ser Ser Ser Ser Phe Ser Ser Pro Ser Ser Ala Gly Arg His
20 25 30

Val Arg Ser Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg Lys Leu
35 40 45

Phe Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly Lys Val
50 55 60

Ser Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu Ile Thr
65 70 75 80

Ser Val Glu Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser Asn Tyr
85 90 95

Tyr Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys Glu Phe
100 105 110

Asn Asn Asp Cys Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly Tyr Asn
115 120 125

Thr Tyr Ala Ser Phe Asn Trp Gln His Asn Gly Arg Gln Met Tyr Val
130 135 140

Ala Leu Asn Gly Lys Gly Ala Pro Arg Arg Gly Gln Lys Thr Arg Arg
145 150 155 160

Lys Asn Thr Ser Ala His Phe Leu Pro Met Val Val His Ser
165 170

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 444 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS

(B) LOCATION: 1..441

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

ATG GCT GGT CGT CAC GTT CGT TCT TAC AAC CAC CTG CAG GGT GAC GTT	48
Met Ala Gly Arg His Val Arg Ser Tyr Asn His Leu Gln Gly Asp Val	
1 5 10 15	
CGT TGG CGT AAA CTG TTC TCT TTC ACC AAA TAC TTC CTG AAA ATC GAA	96
Arg Trp Arg Lys Leu Phe Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu	
20 25 30	
AAA AAC GGT AAA GTT TCT GGG ACC AAG AAC TGC CCG TAC AGC	144
Lys Asn Gly Lys Val Ser Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser	
35 40 45	
ATC CTG GAG ATA ACA TCA GTA GAA ATC GGA GTT GTT GCC GTC AAA GCC	192
Ile Leu Glu Ile Thr Ser Val Glu Ile Gly Val Val Ala Val Lys Ala	
50 55 60	
ATT AAC AGC AAC TAT TAC TTA GCC ATG AAC AAG AAG GGG AAA CTC TAT	240
Ile Asn Ser Asn Tyr Tyr Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr	
65 70 75 80	
GGC TCA AAA GAA TTT AAC AAT GAC TGT AAG CTG AAG GAG AGG ATA GAG	288
Gly Ser Lys Glu Phe Asn Asn Asp Cys Lys Leu Lys Glu Arg Ile Glu	
85 90 95	
GAA AAT GGA TAC AAT ACC TAT GCA TCA TTT AAC TGG CAG CAT AAT GGG	336
Glu Asn Gly Tyr Asn Thr Tyr Ala Ser Phe Asn Trp Gln His Asn Gly	
100 105 110	
AGG CAA ATG TAT GTG GCA TTG AAT GGA AAA GGA GCT CCA AGG AGA GGA	384
Arg Gln Met Tyr Val Ala Leu Asn Gly Lys Gly Ala Pro Arg Arg Gly	
115 120 125	
CAG AAA ACA CGA AGG AAA AAC ACC TCT GCT CAC TTT CTT CCA ATG GTG	432
Gln Lys Thr Arg Arg Lys Asn Thr Ser Ala His Phe Leu Pro Met Val	
130 135 140	
GTA CAC TCA TAG	444
Val His Ser	
145	

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

Met Ala Gly Arg His Val Arg Ser Tyr Asn His Leu Gln Gly Asp Val
1 5 10 15

Arg Trp Arg Lys Leu Phe Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu
20 25 30

Lys Asn Gly Lys Val Ser Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser
35 40 45

Ile Leu Glu Ile Thr Ser Val Glu Ile Gly Val Val Ala Val Lys Ala
50 55 60

Ile Asn Ser Asn Tyr Tyr Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr
65 70 75 80

Gly Ser Lys Glu Phe Asn Asn Asp Cys Lys Leu Lys Glu Arg Ile Glu
85 90 95

Glu Asn Gly Tyr Asn Thr Tyr Ala Ser Phe Asn Trp Gln His Asn Gly
100 105 110

Arg Gln Met Tyr Val Ala Leu Asn Gly Lys Gly Ala Pro Arg Arg Gly
115 120 125

Gln Lys Thr Arg Arg Lys Asn Thr Ser Ala His Phe Leu Pro Met Val
130 135 140

Val His Ser
145

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 402 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..399

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

ATG GTT CGT TGG CGT AAA CTG TTC TCT TTC ACC AAA TAC TTC CTG AAA
Met Val Arg Trp Arg Lys Leu Phe Ser Phe Thr Lys Tyr Phe Leu Lys
1 5 10 15

48

ATC GAA AAA AAC GGT AAA GTT TCT GGG ACC AAG AAG GAG AAC TGC CCG

96

Ile Glu Lys Asn Gly Lys Val Ser Gly Thr Lys Lys Glu Asn Cys Pro			
20	25	30	
TAC AGC ATC CTG GAG ATA ACA TCA GTA GAA ATC GGA GTT GTT GCC GTC			144
Tyr Ser Ile Leu Glu Ile Thr Ser Val Glu Ile Gly Val Val Ala Val			
35	40	45	
AAA GCC ATT AAC AGC AAC TAT TAC TTA GCC ATG AAC AAG AAG GGG AAA			192
Lys Ala Ile Asn Ser Asn Tyr Tyr Leu Ala Met Asn Lys Lys Gly Lys			
50	55	60	
CTC TAT GGC TCA AAA GAA TTT AAC AAT GAC TGT AAG CTG AAG GAG AGG			240
Leu Tyr Gly Ser Lys Glu Phe Asn Asn Asp Cys Lys Leu Lys Glu Arg			
65	70	75	80
ATA GAG GAA AAT GGA TAC AAT ACC TAT GCA TCA TTT AAC TGG CAG CAT			288
Ile Glu Glu Asn Gly Tyr Asn Thr Tyr Ala Ser Phe Asn Trp Gln His			
85	90	95	
AAT GGG AGG CAA ATG TAT GTG GCA TTG AAT GGA AAA GGA GCT CCA AGG			336
Asn Gly Arg Gln Met Tyr Val Ala Leu Asn Gly Lys Gly Ala Pro Arg			
100	105	110	
AGA GGA CAG AAA ACA CGA AGG AAA AAC ACC TCT GCT CAC TTT CTT CCA			384
Arg Gly Gln Lys Thr Arg Arg Lys Asn Thr Ser Ala His Phe Leu Pro			
115	120	125	
ATG GTG GTA CAC TCA TAG			402
Met Val Val His Ser			
130			

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

Met Val Arg Trp Arg Lys Leu Phe Ser Phe Thr Lys Tyr Phe Leu Lys			
1	5	10	15
Ile Glu Lys Asn Gly Lys Val Ser Gly Thr Lys Lys Glu Asn Cys Pro			
20	25	30	
Tyr Ser Ile Leu Glu Ile Thr Ser Val Glu Ile Gly Val Val Ala Val			
35	40	45	
Lys Ala Ile Asn Ser Asn Tyr Tyr Leu Ala Met Asn Lys Lys Gly Lys			
50	55	60	

Leu Tyr Gly Ser Lys Glu Phe Asn Asn Asp Cys Lys Leu Lys Glu Arg
65 70 75 80

Ile Glu Glu Asn Gly Tyr Asn Thr Tyr Ala Ser Phe Asn Trp Gln His
85 90 95

Asn Gly Arg Gln Met Tyr Val Ala Leu Asn Gly Lys Gly Ala Pro Arg
100 105 110

Arg Gly Gln Lys Thr Arg Arg Lys Asn Thr Ser Ala His Phe Leu Pro
115 120 125

Met Val Val His Ser
130

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 354 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..351

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

ATG GAA AAA AAC GGT AAA GTT TCT GGG ACC AAG AAG GAG AAC TGC CCG	48
Met Glu Lys Asn Gly Lys Val Ser Gly Thr Lys Lys Glu Asn Cys Pro	
1 5 10 15	
TAC AGC ATC CTG GAG ATA ACA TCA GTA GAA ATC GGA GTT GTT GCC GTC	96
Tyr Ser Ile Leu Glu Ile Thr Ser Val Glu Ile Gly Val Val Ala Val	
20 25 30	
AAA GCC ATT AAC AGC AAC TAT TAC TTA GCC ATG AAC AAG AAG GGG AAA	144
Lys Ala Ile Asn Ser Asn Tyr Tyr Leu Ala Met Asn Lys Lys Gly Lys	
35 40 45	
CTC TAT GGC TCA AAA GAA TTT AAC AAT GAC TGT AAG CTG AAG GAG AGG	192
Leu Tyr Gly Ser Lys Glu Phe Asn Asn Asp Cys Lys Leu Lys Glu Arg	
50 55 60	
ATA GAG GAA AAT GGA TAC AAT ACC TAT GCA TCA TTT AAC TGG CAG CAT	240
Ile Glu Glu Asn Gly Tyr Asn Thr Tyr Ala Ser Phe Asn Trp Gln His	
65 70 75 80	
AAT GGG AGG CAA ATG TAT GTG GCA TTG AAT GGA AAA GGA GCT CCA AGG	288
Asn Gly Arg Gln Met Tyr Val Ala Leu Asn Gly Lys Gly Ala Pro Arg	

85

90

95

AGA GGA CAG AAA ACA CGA AGG AAA AAC ACC TCT GCT CAC TTT CTT CCA	336	
Arg Gly Gln Lys Thr Arg Arg Lys Asn Thr Ser Ala His Phe Leu Pro		
100	105	110
ATG GTG GTA CAC TCA TAG	354	
Met Val Val His Ser		
115		

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

Met Glu Lys Asn Gly Lys Val Ser Gly Thr Lys Lys Glu Asn Cys Pro			
1	5	10	15
Tyr Ser Ile Leu Glu Ile Thr Ser Val Glu Ile Gly Val Val Ala Val			
20	25	30	
Lys Ala Ile Asn Ser Asn Tyr Tyr Leu Ala Met Asn Lys Lys Gly Lys			
35	40	45	
Leu Tyr Gly Ser Lys Glu Phe Asn Asn Asp Cys Lys Leu Lys Glu Arg			
50	55	60	
Ile Glu Glu Asn Gly Tyr Asn Thr Tyr Ala Ser Phe Asn Trp Gln His			
65	70	75	80
Asn Gly Arg Gln Met Tyr Val Ala Leu Asn Gly Lys Gly Ala Pro Arg			
85	90	95	
Arg Gly Gln Lys Thr Arg Arg Lys Asn Thr Ser Ala His Phe Leu Pro			
100	105	110	
Met Val Val His Ser			
115			

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..318

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

ATG GAG AAC TGC CCG TAC AGC ATC CTG GAG ATA ACA TCA GTA GAA ATC	48
Met Glu Asn Cys Pro Tyr Ser Ile Leu Glu Ile Thr Ser Val Glu Ile	
185 190 195 200	
GGA GTT GTT GCC GTC AAA GCC ATT AAC AGC AAC TAT TAC TTA GCC ATG	96
Gly Val Val Ala Val Lys Ala Ile Asn Ser Asn Tyr Tyr Leu Ala Met	
205 210 215	
AAC AAG AAG GGG AAA CTC TAT GGC TCA AAA GAA TTT AAC AAT GAC TGT	144
Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys Glu Phe Asn Asn Asp Cys	
220 225 230	
AAG CTG AAG GAG AGG ATA GAG GAA AAT GGA TAC AAT ACC TAT GCA TCA	192
Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly Tyr Asn Thr Tyr Ala Ser	
235 240 245	
TTT AAC TGG CAG CAT AAT GGG AGG CAA ATG TAT GTG GCA TTG AAT GGA	240
Phe Asn Trp Gln His Asn Gly Arg Gln Met Tyr Val Ala Leu Asn Gly	
250 255 260	
AAA GGA GCT CCA AGG AGA GGA CAG AAA ACA CGA AGG AAA AAC ACC TCT	288
Lys Gly Ala Pro Arg Arg Gly Gln Lys Thr Arg Arg Lys Asn Thr Ser	
265 270 275 280	
GCT CAC TTT CTT CCA ATG GTG GTA CAC TCA TAG	321
Ala His Phe Leu Pro Met Val Val His Ser	
285 290	

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 amino acids
- (B) TYPE: amino acid
- (C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

Met Glu Asn Cys Pro Tyr Ser Ile Leu Glu Ile Thr Ser Val Glu Ile	
1 5 10 15	
Gly Val Val Ala Val Lys Ala Ile Asn Ser Asn Tyr Tyr Leu Ala Met	
20 25 30	
Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys Glu Phe Asn Asn Asp Cys	

35 40 45
Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly Tyr Asn Thr Tyr Ala Ser
50 55 60
Phe Asn Trp Gln His Asn Gly Arg Gln Met Tyr Val Ala Leu Asn Gly
65 70 75 80
Lys Gly Ala Pro Arg Arg Gly Gln Lys Thr Arg Arg Lys Asn Thr Ser
85 90 95
Ala His Phe Leu Pro Met Val Val His Ser
100 105

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 264 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..261

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

ATG GTC AAA GCC ATT AAC AGC AAC TAT TAC TTA GCC ATG AAC AAG AAG	48
Met Val Lys Ala Ile Asn Ser Asn Tyr Tyr Leu Ala Met Asn Lys Lys	
1 5 10 15	
GGG AAA CTC TAT GGC TCA AAA GAA TTT AAC AAT GAC TGT AAG CTG AAG	96
Gly Lys Leu Tyr Gly Ser Lys Glu Phe Asn Asn Asp Cys Lys Leu Lys	
20 25 30	
GAG AGG ATA GAG GAA AAT GGA TAC AAT ACC TAT GCA TCA TTT AAC TGG	144
Glu Arg Ile Glu Glu Asn Gly Tyr Asn Thr Tyr Ala Ser Phe Asn Trp	
35 40 45	
CAG CAT AAT GGG AGG CAA ATG TAT GTG GCA TTG AAT GGA AAA GGA GCT	192
Gln His Asn Gly Arg Gln Met Tyr Val Ala Leu Asn Gly Lys Gly Ala	
50 55 60	
CCA AGG AGA GGA CAG AAA ACA CGA AGG AAA AAC ACC TCT GCT CAC TTT	240
Pro Arg Arg Gly Gln Lys Thr Arg Arg Lys Asn Thr Ser Ala His Phe	
65 70 75 80	
CTT CCA ATG GTG GTA CAC TCA TAG	264

Leu Pro Met Val Val His Ser
85

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

Met Val Lys Ala Ile Asn Ser Asn Tyr Tyr Leu Ala Met Asn Lys Lys
1 5 10 15

Gly Lys Leu Tyr Gly Ser Lys Glu Phe Asn Asn Asp Cys Lys Leu Lys
20 25 30

Glu Arg Ile Glu Glu Asn Gly Tyr Asn Thr Tyr Ala Ser Phe Asn Trp
35 40 45

Gln His Asn Gly Arg Gln Met Tyr Val Ala Leu Asn Gly Lys Gly Ala
50 55 60

Pro Arg Arg Gly Gln Lys Thr Arg Arg Lys Asn Thr Ser Ala His Phe
65 70 75 80

Leu Pro Met Val Val His Ser
85

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 219 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..216

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

ATG GGG AAA CTC TAT GGC TCA AAA GAA TTT AAC AAT GAC TGT AAG CTG
Met Gly Lys Leu Tyr Gly Ser Lys Glu Phe Asn Asn Asp Cys Lys Leu
1 5 10 15

AAG GAG AGG ATA GAG GAA AAT GGA TAC AAT ACC TAT GCA TCA TTT AAC	96
Lys Glu Arg Ile Glu Glu Asn Gly Tyr Asn Thr Tyr Ala Ser Phe Asn	
20 25 30	
TGG CAG CAT AAT GGG AGG CAA ATG TAT GTG GCA TTG AAT GGA AAA GGA	144
Trp Gln His Asn Gly Arg Gln Met Tyr Val Ala Leu Asn Gly Lys Gly	
35 40 45	
GCT CCA AGG AGA GGA CAG AAA ACA CGA AGG AAA AAC ACC TCT GCT CAC	192
Ala Pro Arg Arg Gly Gln Lys Thr Arg Arg Lys Asn Thr Ser Ala His	
50 55 60	
TTT CTT CCA ATG GTG GTA CAC TCA TAG	219
Phe Leu Pro Met Val Val His Ser	
65 70	

(2) INFORMATION FOR SEQ ID NO:78:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 72 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

Met Gly Lys Leu Tyr Gly Ser Lys Glu Phe Asn Asn Asp Cys Lys Leu	
1 5 10 15	
Lys Glu Arg Ile Glu Glu Asn Gly Tyr Asn Thr Tyr Ala Ser Phe Asn	
20 25 30	
Trp Gln His Asn Gly Arg Gln Met Tyr Val Ala Leu Asn Gly Lys Gly	
35 40 45	
Ala Pro Arg Arg Gly Gln Lys Thr Arg Arg Lys Asn Thr Ser Ala His	
50 55 60	
Phe Leu Pro Met Val Val His Ser	
65 70	

(2) INFORMATION FOR SEQ ID NO:79:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 357 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: both
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 1..357

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

ATG ACC TGC CAG GCT CTG GGT CAG GAC ATG GTT TCT CCG GAA GCT ACC	48
Met Thr Cys Gln Ala Leu Gly Gln Asp Met Val Ser Pro Glu Ala Thr	
1 5 10 15	
AAC TCT TCC TCT TCC TTC TCT TCC CCG TCT TCC GCT GGT CGT CAC	96
Asn Ser Ser Ser Ser Phe Ser Ser Pro Ser Ser Ala Gly Arg His	
20 25 30	
GTT CGT TCT TAC AAC CAC CTG CAG GGT GAC GTT CGT TGG CGT AAA CTG	144
Val Arg Ser Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg Lys Leu	
35 40 45	
TTC TCT TTC ACC AAA TAC TTC CTG AAA ATC GAA AAA AAC GGT AAA GTT	192
Phe Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly Lys Val	
50 55 60	
TCT GGG ACC AAG AAG GAG AAC TGC CCG TAC AGC ATC CTG GAG ATA ACA	240
Ser Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu Ile Thr	
65 70 75 80	
TCA GTA GAA ATC GGA GTT GTT GCC GTC AAA GCC ATT AAC AGC AAC TAT	288
Ser Val Glu Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser Asn Tyr	
85 90 95	
TAC TTA GCC ATG AAC AAG AAG GGG AAA CTC TAT GGC TCA AAA GAA TTT	336
Tyr Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys Glu Phe	
100 105 110	
AAC AAT GAC TGT AAG CTG AAG	357
Asn Asn Asp Cys Lys Leu Lys	
115	

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 119 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

Met Thr Cys Gln Ala Leu Gly Gln Asp Met Val Ser Pro Glu Ala Thr	
1 5 10 15	
Asn Ser Ser Ser Ser Phe Ser Ser Pro Ser Ser Ala Gly Arg His	
20 25 30	

Val Arg Ser Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg Lys Leu
35 40 45

Phe Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly Lys Val
50 55 60

Ser Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu Ile Thr
65 70 75 80

Ser Val Glu Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser Asn Tyr
85 90 95

Tyr Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys Glu Phe
100 105 110

Asn Asn Asp Cys Lys Leu Lys
115

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..276

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

ATG GCT GGT CGT CAC GTT CGT TCT TAC AAC CAC CTC CAG GGT GAC GTT 48
Met Ala Gly Arg His Val Arg Ser Tyr Asn His Leu Gln Gly Asp Val
1 5 10 15

CGT TGG CGT AAA CTG TTC TCT ACC AAA TAC TTC CTG AAA ATC GAA 96
Arg Trp Arg Lys Leu Phe Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu
20 25 30

AAA AAC GGT AAA GTT TCT GGG ACC AAG AAG GAG AAC TGC CCG TAC AGC 144
Lys Asn Gly Lys Val Ser Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser
35 40 45

ATC CTG GAG ATA ACA TCA GTA GAA ATC GGA GTT GTT GCC GTC AAA GCC 192
Ile Leu Glu Ile Thr Ser Val Glu Ile Gly Val Val Ala Val Lys Ala
50 55 60

ATT AAC AGC AAC TAT TAC TTA GCC ATG AAC AAG AAG GGG AAA CTC TAT 240
Ile Asn Ser Asn Tyr Tyr Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr
65 70 75 80

GGC TCA AAA GAA TTT AAC AAT GAC TGT AAG CTG AAG
Gly Ser Lys Glu Phe Asn Asn Asp Cys Lys Leu Lys
85 90

276

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 92 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

Met Ala Gly Arg His Val Arg Ser Tyr Asn His Leu Gln Gly Asp Val
1 5 10 15

Arg Trp Arg Lys Leu Phe Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu
20 25 30

Lys Asn Gly Lys Val Ser Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser
35 40 45

Ile Leu Glu Ile Thr Ser Val Glu Ile Gly Val Val Ala Val Lys Ala
50 55 60

Ile Asn Ser Asn Tyr Tyr Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr
65 70 75 80

Gly Ser Lys Glu Phe Asn Asn Asp Cys Lys Leu Lys
85 90

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 525 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

ATGACCTCTC AGGCTCTGGG TCAGGACATG GTTTCTCCGG AAGCTACCAA CTCTTCCTCT 60
TCCTCTTTCT CTTCCCCGTC TTCCGCTGGT CGTCACGTTG GTTCTTACAA CCACCTGCAG 120
GGTGACGTTG GTTGGCGTAA ACTGTTCTCT TTCACCAAAT ACTTCCTGAA AATCGAAAAA 180

AACGGTAAAG TTTCTGGAC CAAGAAGGAG AACTCTCCGT ACAGCATCCT GGAGATAACA	240
TCAGTAGAAA TCGGAGTTGT TGCCGTAAA GCCATTAACA GCAACTATTA CTTAGCCATG	300
AACAAGAAGG GGAAACTCTA TGGCTCAAAA GAATTAAACA ATGACTGTAA GCTGAAGGAG	360
AGGATAGAGG AAAATGGATA CAATACCTAT GCATCATTAA ACTGGCAGCA TAATGGGAGG	420
CAAATGTATG TGGCATTGAA TGGAAAAGGA GCTCCAAGGA GAGGACAGAA AACACGAAGG	480
AAAAACACCT CTGCTCACTT TCTTCCAATG GTGGTACACT CATAG	525

(2) INFORMATION FOR SEQ ID NO:84:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 525 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: both
- (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

ATGACCTGCC AGGCTCTGGG TCAGGACATG GTTCTCCGG AAGCTACCAA CTCTTCCTCT	60
TCCTCTTTCT CTTCCCCGTC TTCCGCTGGT CGTCACGTTC GTTCTTACAA CCACCTGCAG	120
GGTGACGTTC GTTGGCGTAA ACTGTTCTCT TTCAACCAAT ACTTCCTGAA AATCGAAAAA	180
AACGGTAAAG TTTCTGGAC CAAGAAGGAG AACTCTCCGT ACAGCATCCT GGAGATAACA	240
TCAGTAGAAA TCGGAGTTGT TGCCGTAAA GCCATTAACA GCAACTATTA CTTAGCCATG	300
AACAAGAAGG GGAAACTCTA TGGCTCAAAA GAATTAAACA ATGACTGTAA GCTGAAGGAG	360
AGGATAGAGG AAAATGGATA CAATACCTAT GCATCATTAA ACTGGCAGCA TAATGGGAGG	420
CAAATGTATG TGGCATTGAA TGGAAAAGGA GCTCCAAGGA GAGGACAGAA AACACGAAGG	480
AAAAACACCT CTGCTCACTT TCTTCCAATG GTGGTACACT CATAG	525

(2) INFORMATION FOR SEQ ID NO:85:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

GGACCCTCAT GACCTCTCAG GCTCTGGGT

29

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

AAGGAGAACT CTCCGTACAG C

21

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

GCTGTACGGT CTGTTCTCCT T

21

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

GGACCCTCAT GACCTGCCAG GCTCTGGGTC AGGAC

35

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

CTGCCCAAGC TTATTATGAG TGTACCACCA TTGGAAG

37

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

AAAGGATCCT GCCAGGCTCT GGGTCAGGAC ATG

33

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

GCGGCACATG TCTTACAACC ACCTGCAGGG TG

32

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

GGGCCCAAGC TTATGAGTGT ACCACCAT

28

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

CCGGCGGATC CCATATGTCT TACAACCACC TGCAGG

36

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

CCGGCGGTAC CTTATTATGA GTGTACCACC ATTGG

35

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

ATGTCTTACA ACCACCTGCA GGGTGACGTT CGTTGGCGTA AACTGTTCTC TTTCACCAAA	60
TACTTCCTGA AAATCGAAAA AAACGGTAAA GTTTCTGGGA CCAAGAAGGA GAACTGCCCG	120
TACAGCATCC TGGAGATAAC ATCAGTAGAA ATCGGAGTTG TTGCCGTCAA AGCCATTAAC	180
AGCAACTATT ACTTAGCCAT GAACAAGAAG GGGAAACTCT ATGGCTAAA AGAATTTAAC	240
AATGACTGTA AGCTGAAGGA GAGGATAGAG GAAAATGGAT ACAATACCTA TGCATCATT	300
AACTGGCAGC ATAATGGGAG GCAAATGTAT GTGGCATTGA ATGGAAAAGG AGCTCCAAGG	360
AGAGGACAGA AAACACGAAG GAAAAACACC TCTGCTCACT TTCTTCCAAT GGTGGTACAC	420
TCATAA	426

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

Met Ser Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg Lys Leu Phe			
1	5	10	15
Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly Lys Val Ser			
20	25	30	
Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu Ile Thr Ser			
35	40	45	
Val Glu Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser Asn Tyr Tyr			
50	55	60	
Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys Glu Phe Asn			
65	70	75	80

Asn Asp Cys Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly Tyr Asn Thr
85 90 95

Tyr Ala Ser Phe Asn Trp Gln His Asn Gly Arg Gln Met Tyr Val Ala
100 105 110

Leu Asn Gly Lys Gly Ala Pro Arg Arg Gly Gln Lys Thr Arg Arg Lys
115 120 125

Asn Thr Ser Ala His Phe Leu Pro Met Val Val His Ser
130 135 140

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

CAACCACCTG CAGGGTGACG 20

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

AACGGTCGAC AAATGTATGT GGCACTGAAC GGTAAAGGTG CTCCACGTCG TGGTCAGAAA 60

ACCCGTCGTA AAAACACC 78

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

GGGCCCAAGC TTAAGAGTGT ACCACCATTG GCAGAAAGTG AGCAGAGGTG TTTTTACGAC	60
GGGTTTTCTG ACCACG	76

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

GCCACATACA TTTGTCGACC GTT	23
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(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

GGGCCCAAGC TTAAGAGTG	19
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(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

GCCACATACA TTTGTCGACC GTT

23

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

CTGCAGGGTG ACGTCGTTG GCGTAAACTG TTCTCCTTCA CCAAATACCTT CCTGAAAATC

60

GAAAAAAAACG GTAAAGTTTC TGGTACCAAG

90

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

AGCTTTAACCA GCAACAAACAC CGATTCAAC GGAGGTGATT TCCAGGATGG AGTACGGGCA

60

GTTTTCTTTC TTGGTACCAAG AAACTTTACC

90

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

GGTGTGTTG CTGTTAAAGC TATCAACTCC AACTACTACC TGGCTATGAA CAAGAAAGGT 60
AAACTGTACG GTTCCAAAGA ATTTAACAAAC 90

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

GTCGACCGTT GTGCTGCCAG TTGAAGGAAG CGTAGGTGTT GTAACCGTTT TCTTCGATAAC 60
GTTCTTTCAG TTTACAGTCG TTGTTAAATT CTTTGGAAC 100

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

GCGGCCTCGA CCGTTGTGCT GCCAG 25

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

GCGGCCTGCA GGGTGACGTT CGTTGG

26

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

CCGGCGGATC CCATATGTCT TACAACCACC TGCAGG

36

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

CGCGCGATAT CTTATTAAGA GTGTACCACC ATTG

34

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

ATGTCTTACA ACCACCTGCA GGGTGACGTT CGTTGGCGTA AACTGTTCTC CTTCACCAAA

60

TACTTCCTGA AAATCGAAAA AAACGGTAAA GTTTCTGGTA CCAAGAAAGA AAACTGCCCG	120
TACTCCATCC TGGAAATCAC CTCCGTTGAA ATCGGTGTTG TTGCTGTTAA AGCTATCAAC	180
TCCAACACT ACCTGGCTAT GAACAAGAAA GGTAAACTGT ACGGTTCCAA AGAATTAAAC	240
AACGACTGTA AACTGAAAGA ACGTATCGAA GAAAACGGTT ACAACACCTA CGCTTCCTTC	300
AACTGGCAGC ACAACGGTCG ACAAAATGTAT GTGGCACTGA ACGGTAAAGG TGCTCCACGT	360
CGTGGTCAGA AAACCCGTCG TAAAAACACC TCTGCTCACT TTCTGCCAAT GGTGGTACAC	420
TCTTAA	426

(2) INFORMATION FOR SEQ ID NO:112:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 141 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: not relevant
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

Met Ser Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg Lys Leu Phe			
1	5	10	15
Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly Lys Val Ser			
20	25	30	
Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu Ile Thr Ser			
35	40	45	
Val Glu Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser Asn Tyr Tyr			
50	55	60	
Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys Glu Phe Asn			
65	70	75	80
Asn Asp Cys Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly Tyr Asn Thr			
85	90	95	
Tyr Ala Ser Phe Asn Trp Gln His Asn Gly Arg Gln Met Tyr Val Ala			
100	105	110	
Leu Asn Gly Lys Gly Ala Pro Arg Arg Gly Gln Lys Thr Arg Arg Lys			
115	120	125	
Asn Thr Ser Ala His Phe Leu Pro Met Val Val His Ser			
130	135	140	

(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

CGCGGCCATG GCTCTGGTC AGGACATG

28

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

GGGCCAAGC TTATGAGTGT ACCACCAT

28

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 516 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

ATGGCTCTGG GTCAAGATAT GGTTTCTCCG GAAGCTACCA ACTCTTCCTC TTCCCTTTTC

60

TCTTCCCCGT CTTCCGCTGG TCGTCACGTT CGTTCTTACA ACCACCTGCA GGGTGACGTT

120

CGTTGGCGTA AACTGTTCTC TTTCACCAAA TACTTCCTGA AAATCGAAAA AAACGGTAAA

180

GTTCCTGGGA CCAAGAAGGA GAACTGCCCG TACAGCATCC TGGAGATAAC ATCAGTAGAA	240
ATCGGAGTTG TTGCCGTCAA AGCCATTAAC AGCAACTATT ACTTAGCCAT GAACAAGAAG	300
GGGAAACTCT ATGGCTCAAA AGAATTTAAC AATGACTGTA AGCTGAAGGA GAGGATAGAG	360
GAAAATGGAT ACAATACCTA TGCATCATT AACTGGCAGC ATAATGGGAG GCAAATGTAT	420
GTGGCATTGA ATGGAAAAGG AGCTCCAAGG AGAGGACAGA AAACACGAAG GAAAAACACC	480
TCTGCTCACT TTCTTCCAAT GGTGGTACAC TCATAA	516

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 171 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

Met Ala Leu Gly Gln Asp Met Val Ser Pro Glu Ala Thr Asn Ser Ser
1 5 10 15

Ser Ser Ser Phe Ser Ser Pro Ser Ser Ala Gly Arg His Val Arg Ser
20 25 30

Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg Lys Leu Phe Ser Phe
35 40 45

Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly Lys Val Ser Gly Thr
50 55 60

Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu Ile Thr Ser Val Glu
65 70 75 80

Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser Asn Tyr Tyr Leu Ala
85 90 95

Met Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys Glu Phe Asn Asn Asp
100 105 110

Cys Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly Tyr Asn Thr Tyr Ala
115 120 125

Ser Phe Asn Trp Gln His Asn Gly Arg Gln Met Tyr Val Ala Leu Asn
130 135 140

Gly Lys Gly Ala Pro Arg Arg Gly Gln Lys Thr Arg Arg Lys Asn Thr

145	150	155	160
Ser Ala His Phe Leu Pro Met Val Val His Ser			
	165	170	

(2) INFORMATION FOR SEQ ID NO:117:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

GCAGGCACATG TCTTACAACC ACCTGCAGGG TG 32

(2) INFORMATION FOR SEQ ID NO:118:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 75 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

CTGCCCAAGC TTTTATGAGT GTACCACCAT TGGAAGAAAG TGAGCAGAGG TGTTTTTTC 60

TCGTGTTTTC TGTCC 75

(2) INFORMATION FOR SEQ ID NO:119:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 426 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

ATGTCTTACA ACCACCTGCA GGGTGACGTT CGTTGGCGTA AACTGTTCTC TTTCACCAAA	60
TACTTCCTGA AAATCGAAAA AAACGGTAAA GTTCTGGGA CCAAGAAGGA GAACTGCCCG	120
TACAGCATCC TGGAGATAAC ATCAGTAGAA ATCGGAGTTG TTGCCGTCAA AGCCATTAAC	180
AGCAACTATT ACTTAGCCAT GAACAAGAAG GGGAAACTCT ATGGCTAAA AGAATTTAAC	240
AATGACTGTA AGCTGAAGGA GAGGATAGAG GAAAATGGAT ACAATACCTA TGCATCATT	300
AACTGGCAGC ATAATGGGAG GCAAATGTAT GTGGCATTGA ATGGAAAAGG AGCTCCAAGG	360
AGAGGACAGA AAACACGAGA AAAAAACACC TCTGCTCACT TTCTTCCAAT GGTGGTACAC	420
TCATAG	426

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

Met Ser Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg Lys Leu Phe			
1	5	10	15
Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly Lys Val Ser			
20	25	30	
Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu Ile Thr Ser			
35	40	45	
Val Glu Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser Asn Tyr Tyr			
50	55	60	
Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys Glu Phe Asn			
65	70	75	80
Asn Asp Cys Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly Tyr Asn Thr			
85	90	95	
Tyr Ala Ser Phe Asn Trp Gln His Asn Gly Arg Gln Met Tyr Val Ala			
100	105	110	
Leu Asn Gly Lys Gly Ala Pro Arg Arg Gly Gln Lys Thr Arg Glu Lys			
115	120	125	

Asn Thr Ser Ala His Phe Leu Pro Met Val Val His Ser
130 135 140

(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

GCGGCACATG TCTTACAACC ACCTGCAGGG TG 32

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 75 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

CTGCCCAAGC TTTTATGAGT GTACCACCAT TGGAAGAAAG TGAGCAGAGG TGTTTTCTG 60

TCGTGTTTTC TGTCC 75

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 426 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

ATGTCTTACA ACCACCTGCA GGGTGACGTT CGTTGGCGTA AACTGTTCTC TTTCACCAAA 60

TACTTCCTGA AAATCGAAAA AAACGGTAAA GTTTCTGGGA CCAAGAAGGA GAACTGCCCG	120
TACAGCATCC TGGAGATAAC ATCAGTAGAA ATCGGAGTTG TTGCCGTCAA AGCCATTAAC	180
AGCAACTATT ACTTAGCCAT GAACAAGAAG GGGAAACTCT ATGGCTCAA AGAATTAAAC	240
AATGACTGTA AGCTGAAGGA GAGGATAGAG GAAAATGGAT ACAATACCTA TGCATCATT	300
AACTGGCAGC ATAATGGGAG GCAAATGTAT GTGGCATTGA ATGGAAAAGG AGCTCCAAGG	360
AGAGGACAGA AAACACGACA GAAAAACACC TCTGCTCACT TTCTTCCAAT GGTGGTACAC	420
TCATAG	426

(2) INFORMATION FOR SEQ ID NO:124:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 141 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: not relevant
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

Met Ser Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg Lys Leu Phe			
1	5	10	15
Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly Lys Val Ser			
20	25	30	
Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu Ile Thr Ser			
35	40	45	
Val Glu Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser Asn Tyr Tyr			
50	55	60	
Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys Glu Phe Asn			
65	70	75	80
Asn Asp Cys Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly Tyr Asn Thr			
85	90	95	
Tyr Ala Ser Phe Asn Trp Gln His Asn Gly Arg Gln Met Tyr Val Ala			
100	105	110	
Leu Asn Gly Lys Gly Ala Pro Arg Arg Gly Gln Lys Thr Arg Gln Lys			
115	120	125	
Asn Thr Ser Ala His Phe Leu Pro Met Val Val His Ser			
130	135	140	

(2) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

GCGGCACATG TCTTACAACC ACCTGCAGGG TG

32

(2) INFORMATION FOR SEQ ID NO:126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

CTGCCAAGC TTTTATGAGT GTACCACCAT TGGAAGAAAG TGAGCAGAGG TGTTTTCCCT

60

TCGTGTTCC TGTCCCTCTCC TTGG

84

(2) INFORMATION FOR SEQ ID NO:127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

ATGTCTTACA ACCACCTGCA GGGTGACGTT CGTTGGCGTA AACTGTTCTC TTTCACCAAA

60

TACTTCCTGA AAATCGAAAAA AAACGGTAAA GTTTCTGGGA CCAAGAAGGA GAACTGCCCG

120

TACAGCATCC	TGGAGATAAC	ATCAGTAGAA	ATCGGAGTTG	TTGCCGTCAA	AGCCATTAAC	180
AGCAACTATT	ACTTAGCCAT	GAACAAGAAG	GGGAAACTCT	ATGGCTCAA	AGAATTAAAC	240
AATGACTGTA	AGCTGAAGGA	GAGGATAGAG	GAAAATGGAT	ACAATACCTA	TGCATCATT	300
AACTGGCAGC	ATAATGGGAG	GCAAATGTAT	GTGGCATTGA	ATGGAAAAGG	AGCTCCAAGG	360
AGAGGACAGG	AAACACGAAG	GAAAACACC	TCTGCTCACT	TTCTTCCAAT	GGTGGTACAC	420
TCATAG						426

(2) INFORMATION FOR SEQ ID NO:128:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

Met	Ser	Tyr	Asn	His	Leu	Gln	Gly	Asp	Val	Arg	Trp	Arg	Lys	Leu	Phe
1					5				10					15	
Ser	Phe	Thr	Lys	Tyr	Phe	Leu	Lys	Ile	Glu	Lys	Asn	Gly	Lys	Val	Ser
					20			25					30		
Gly	Thr	Lys	Lys	Glu	Asn	Cys	Pro	Tyr	Ser	Ile	Leu	Glu	Ile	Thr	Ser
					35			40					45		
Val	Glu	Ile	Gly	Val	Val	Ala	Val	Lys	Ala	Ile	Asn	Ser	Asn	Tyr	Tyr
					50			55					60		
Leu	Ala	Met	Asn	Lys	Lys	Gly	Lys	Leu	Tyr	Gly	Ser	Lys	Glu	Phe	Asn
					65			70					75		80
Asn	Asp	Cys	Lys	Leu	Lys	Glu	Arg	Ile	Glu	Glu	Asn	Gly	Tyr	Asn	Thr
					85				90					95	
Tyr	Ala	Ser	Phe	Asn	Trp	Gln	His	Asn	Gly	Arg	Gln	Met	Tyr	Val	Ala
					100			105					110		
Leu	Asn	Gly	Lys	Gly	Ala	Pro	Arg	Arg	Gly	Gln	Glu	Thr	Arg	Arg	Lys
					115			120					125		
Asn	Thr	Ser	Ala	His	Phe	Leu	Pro	Met	Val	Val	His	Ser			
					130			135					140		

(2) INFORMATION FOR SEQ ID NO:129:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

GCAGGCACATG TCTTACAACC ACCTGCAGGG TG 32

(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 84 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

CTGCCCCAAGC TTTTATGAGT GTACCACCAT TGGAAGAAAG TGAGCAGAGG TGTTTTTCCT 60

TCGTGTCTGC TGTCCCTCTCC TTGG 84

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 426 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

ATGTCTTACA ACCACCTGCA GGGTGACGTT CGTTGGCGTA AACTGTTCTC TTTCACCAAA 60

TACTTCCTGA AAATCGAAAA AAACGGTAAA GTTTCTGGGA CCAAGAAGGA GAACTGCCCG 120

TACAGCATCC TGGAGATAAC ATCAGTAGAA ATCGGAGTTG TTGCCGTCAA AGCCATTAAC 180

AGCAACTATT ACTTAGCCAT GAACAAGAAG GGGAAACTCT ATGGCTCAA AGAATTTAAC	240
AATGACTGTA AGCTGAAGGA GAGGATAGAG GAAAATGGAT ACAATACCTA TGCATCATT	300
AACTGGCAGC ATAATGGGAG GCAAATGTAT GTGGCATTGA ATGGAAAAGG AGCTCCAAGG	360
AGAGGACAGC AGACACGAAG GAAAAACACC TCTGCTCACT TTCTTCCAAT GGTGGTACAC	420
TCATAG	426

(2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

Met Ser Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg Lys Leu Phe			
1	5	10	15
Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly Lys Val Ser			
20	25	30	
Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu Ile Thr Ser			
35	40	45	
Val Glu Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser Asn Tyr Tyr			
50	55	60	
Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys Glu Phe Asn			
65	70	75	80
Asn Asp Cys Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly Tyr Asn Thr			
85	90	95	
Tyr Ala Ser Phe Asn Trp Gln His Asn Gly Arg Gln Met Tyr Val Ala			
100	105	110	
Leu Asn Gly Lys Gly Ala Pro Arg Arg Gly Gln Gln Thr Arg Arg Lys			
115	120	125	
Asn Thr Ser Ala His Phe Leu Pro Met Val Val His Ser			
130	135	140	

(2) INFORMATION FOR SEQ ID NO:133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

CGGGCACATG TCTTACAACC ACCTGCAGGG TG 32

(2) INFORMATION FOR SEQ ID NO:134:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 93 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

CTGCCCAAGC TTTTATGAGT GTACCACCAT TGGAAGAAAG TGAGCAGAGG TGTTTTTCCT 60

TCGTGTTTTC TGTCTTCCC TTGGAGCTCC TTT 93

(2) INFORMATION FOR SEQ ID NO:135:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 426 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

ATGTCTTACA ACCACCTGCA GGGTGACGTT CGTTGGCGTA AACTGTTCTC TTTCACCAAA 60

TACTTCCTGA AAATCGAAAA AAACGGTAAA GTTTCTGGGA CCAAGAAGGA GAACTGCCCG 120

TACAGCATCC TGGAGATAAC ATCAGTAGAA ATCGGAGTTG TTGCCGTCAA AGCCATTAAC 180

AGCAACTATT ACTTAGCCAT GAACAAGAAG GGGAAACTCT ATGGCTCAAA AGAATTAAAC 240

AATGACTGTA AGCTGAAGGA GAGGATAGAG GAAAATGGAT ACAATACCTA TGCATCATT	300
AACTGGCAGC ATAATGGGAG GCAAATGTAT GTGGCATTGA ATGGAAAAGG AGCTCCAAGG	360
GAAGGACAGA AAACACGAAG GAAAAACACC TCTGCTCACT TTCTTCCAAT GGTGGTACAC	420
TCATAG	426

(2) INFORMATION FOR SEQ ID NO:136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

Met Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg Lys Leu Phe Ser			
1	5	10	15
Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly Lys Val Ser Gly			
20	25	30	
Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu Ile Thr Ser Val			
35	40	45	
Glu Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser Asn Tyr Tyr Leu			
50	55	60	
Ala Met Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys Glu Phe Asn Asn			
65	70	75	80
Asp Cys Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly Tyr Asn Thr Tyr			
85	90	95	
Ala Ser Phe Asn Trp Gln His Asn Gly Arg Gln Met Tyr Val Ala Leu			
100	105	110	
Asn Gly Lys Gly Ala Pro Arg Glu Gly Gln Lys Thr Arg Arg Lys Asn			
115	120	125	
Thr Ser Ala His Phe Leu Pro Met Val Val His Ser			
130	135	140	

(2) INFORMATION FOR SEQ ID NO:137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

CGGGCACATG TCTTACAACC ACCTGCAGGG TG

32

(2) INFORMATION FOR SEQ ID NO:138:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 93 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

CTGCCCAAGC TTTTATGAGT GTACCACCAT TGGAAGAAAG TGAGCAGAGG TGTTTTTCCT

60

TCGTGTTTC TGTCCCTGCC TTGGAGCTCC TTT

93

(2) INFORMATION FOR SEQ ID NO:139:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 426 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

ATGTCTTACA ACCACCTGCA GGGTGACGTT CGTTGGCGTA AACTGTTCTC TTTCACCAAA

60

TACTTCCTGA AAATCGAAAA AAACGGTAAA GTTTCTGGGA CCAAGAAGGA GAACTGCCCG

120

TACAGCATCC TGGAGATAAC ATCAGTAGAA ATCGGAGTTG TTGCCGTCAA AGCCATTAAC

180

AGCAACTATT ACTTAGCCAT GAACAAGAAG GGGAAACTCT ATGGCTCAA AGAATTAAAC

240

AATGACTGTA AGCTGAAGGA GAGGATAGAG GAAAATGGAT ACAATACCTA TGCATCATTT

300

AACTGGCAGC ATAATGGGAG GCAAATGTAT GTGGCATTGA ATGGAAAAGG AGCTCCAAGG	360
CAGGGACAGA AAACACGAAG GAAAAACACC TCTGCTCACT TTCTTCCAAT GGTGGTACAC	420
TCATAG	426

(2) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

Met Ser Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg Lys Leu Phe			
1	5	10	15
Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly Lys Val Ser			
20	25	30	
Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu Ile Thr Ser			
35	40	45	
Val Glu Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser Asn Tyr Tyr			
50	55	60	
Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys Glu Phe Asn			
65	70	75	80
Asn Asp Cys Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly Tyr Asn Thr			
85	90	95	
Tyr Ala Ser Phe Asn Trp Gln His Asn Gly Arg Gln Met Tyr Val Ala			
100	105	110	
Leu Asn Gly Lys Gly Ala Pro Arg Gln Gly Gln Lys Thr Arg Arg Lys			
115	120	125	
Asn Thr Ser Ala His Phe Leu Pro Met Val Val His Ser			
130	135	140	

(2) INFORMATION FOR SEQ ID NO:141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

GCAGCACATG TCTTACAACC ACCTGCAGGG TG

32

(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

TTGAATGGAG AAGGAGCTCC A

21

(2) INFORMATION FOR SEQ ID NO:143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

TGGAGCTCCT TCTCCATTCA A

21

(2) INFORMATION FOR SEQ ID NO:144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

CTGCCCAAGC TTTTATGAGT GTACCACCAT TGG 33

(2) INFORMATION FOR SEQ ID NO:145:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

ATGTCTTACA ACCACCTGCA GGGTGACGTT CGTTGGCGTA AACTGTTCTC TTTCACCAAA	60
TACTTCCTGA AAATCGAAAA AAACGGTAAA GTTTCTGGGA CCAAGAAGGA GAACTGCCCG	120
TACAGCATCC TGGAGATAAC ATCAGTAGAA ATCGGAGTTG TTGCCGTCAA AGCCATTAAC	180
AGCAACTATT ACTTAGCCAT GAACAAGAAG GGGAAACTCT ATGGCTCAA AGAATTAAAC	240
AATGACTGTA AGCTGAAGGA GAGGATAGAG GAAAATGGAT ACAATACCTA TGCATCATT	300
AACTGGCAGC ATAATGGGAG GCAAATGTAT GTGGCATTGA ATGGAGAAGG AGCTCCAAGG	360
AGAGGACAGA AAACACGAAG GAAAAACACC TCTGCTCACT TTCTTCCAAT GGTGGTACAC	420
TCATAG	426

(2) INFORMATION FOR SEQ ID NO:146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

Met Ser Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg Lys Leu Phe			
1	5	10	15

Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly Lys Val Ser		
20	25	30

Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu Ile Thr Ser
35 40 45

Val Glu Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser Asn Tyr Tyr
50 55 60

Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys Glu Phe Asn
65 70 75 80

Asn Asp Cys Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly Tyr Asn Thr
85 90 95

Tyr Ala Ser Phe Asn Trp Gln His Asn Gly Arg Gln Met Tyr Val Ala
100 105 110

Leu Asn Gly Glu Gly Ala Pro Arg Arg Gly Gln Lys Thr Arg Arg Lys
115 120 125

Asn Thr Ser Ala His Phe Leu Pro Met Val Val His Ser
130 135 140

(2) INFORMATION FOR SEQ ID NO:147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3974 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

GGTACCTAAG TGAGTAGGGC GTCCGATCGA CGGACGCCTT TTTTTGAAT TCGTAATCAT	60
GGTCATAGCT GTTTCCTGTG TGAAATTGTT ATCCGCTCAC AATTCCACAC AACATACGAG	120
CCGGAAGCAT AAAGTGTAAA GCCTGGGGTG CCTAATGAGT GAGCTAACTC ACATTAATTG	180
CGTTGCGCTC ACTGCCCGCT TTCCAGTCGG GAAACCTGTC GTGCCAGCTG CATTAATGAA	240
TCGGCCAACG CGCGGGGAGA GGCGGTTTGC GTATTGGCG CTCTTCCGCT TCCTCGCTCA	300
CTGACTCGCT GCGCTCGGTC GTTCGGCTGC GGCGAGCGGT ATCAGCTCAC TCAAAGGCCG	360
TAATACGGTT ATCCACAGAA TCAGGGATA ACGCAGGAAA GAACATGTGA GCAAAAGGCC	420
AGCAAAAGGC CAGGAACCGT AAAAAGGCCG CGTTGCTGGC GTTTTCCAT AGGCTCCGCC	480
CCCCCTGACGA GCATCACAAA AATCGACGCT CAAGTCAGAG GTGGCGAAC CCGACAGGAC	540

TATAAAAGATA CCAGGCCTTT	CCCCCTGGAA GCTCCCTCGT	GCGCTCTCCT GTTCCGACCC	600
TGCCGCTTAC CGGATAACCTG	TCCGCCTTTC TCCCTTCGGG	AAGCGTGGCG CTTTCTCATA	660
GCTCACGCTG TAGGTATCTC	AGTCGGTGT AGGTCGTTCG	CTCCAAGCTG GGCTGTGTGC	720
ACGAACCCCC CGTTCAGCCC	GACCGCTGCG CCTTATCCGG	TAACTATCGT CTTGAGTCCA	780
ACCCGGTAAG ACACGACTTA	TCGCCACTGG CAGCAGCCAC	TGGTAACAGG ATTAGCAGAG	840
CGAGGGTATGT AGGCGGTGCT	ACAGAGTTCT TGAAGTGGTG	GCCTAACTAC GGCTACACTA	900
GAAGAACAGT ATTTGGTATC	TGCGCTCTGC TGAAGCCAGT	TACCTTCGGA AAAAGAGTTG	960
GTAGCTCTTG ATCCGGCAAA	CAAACCACCG CTGGTAGCGG	TGGTTTTTTT GTTGCAAGC	1020
AGCAGATTAC GCGCAGAAAA	AAAGGATCTC AAGAAGATCC	TTTGATCTTT TCTACGGGGT	1080
CTGACGCTCA GTGGAACGAA	AACTCACGTT AAGGGATTTT	GGTCATGAGA TTATCGTCGA	1140
CAATTCGCGC GCGAAGGCGA	ACCGGCATGC ATTTACGTTG	ACACCATCGA ATGGTGCAAA	1200
ACCTTCGCG GTATGGCATG	ATAGCGCCCG GAAGAGAGTC	AATTCAAGGGT GGTGAATGTG	1260
AAACCAGTAA CGTTATACGA	TGTCGCAGAG TATGCCGGTG	TCTCTTATCA GACC GTTTCC	1320
CGCGTGGTGA ACCAGGCCAG	CCACGTTCT GCGAAAACGC	GGGAAAAAGT GGAAGCGGCG	1380
ATGGCGGAGC TGAATTACAT	TCCCAACCAGC GTGGCACAAC	AACTGGCGGG CAAACAGTCG	1440
TTGCTGATTG GCGTTGCCAC	CTCCAGTCTG GCCCTGCACG	CGCCGTCGCA AATTGTCGCG	1500
GCGATTAAAT CTCGCGCCGA	TCAACTGGGT GCCAGCGTGG	TGGTGTGCGAT GGTAGAACGA	1560
AGCGGCGTCG AAGCCTGTAA	AGCGGCGGTG CACAATCTTC	TCGCGCAACG CGTCAGTGGG	1620
CTGATCATTA ACTATCCGCT	GGATGACCAAG GATGCCATTG	CTGTGGAAGC TGCCTGCACT	1680
AATGTTCCGG CGTTATTTCT	TGATGTCTCT GACCAGACAC	CCATCAACAG TATTATTTTC	1740
TCCCATGAAG ACGGTACGCG	ACTGGCGTG GAGCATCTGG	TCGCATTGGG TCACCAGCAA	1800
ATCGCGCTGT TAGCGGGCCC	ATTAAGTTCT GTCTCGCGC	GTCTCGGTCT GGCTGGCTGG	1860
CATAAAATATC TCACTCGAA	TCAAATTCAAG CCGATAGCGG	AACGGGAAGG CGACTGGAGT	1920
GCCATGTCCG GTTTCAACA	AACCATGCAA ATGCTGAATG	AGGGCATCGT TCCCCTGCG	1980
ATGCTGGTTG CCAACGATCA	GATGGCGCTG GGCGCAATGC	GCGCCATTAC CGAGTCCGGG	2040
CTGCGCGTTG GTGCGGATAT	CTCGGTAGTG GGATACGACG	ATACCGAAGA CAGCTCATGT	2100
TATATCCCGC CGTTAACACAC	CATCAAACAG GATTTCGCC	TGCTGGGGCA AACCAAGCGTG	2160
GACCGCTTGC TGCAACTCTC	TCAGGGCCAG GCGGTGAAGG	GCAATCAGCT GTTGCCCGTC	2220

TCACTGGTGA AAAGAAAAAC CACCTGGCG CCCAATACGC AAACCGCCTC TCCCCGCGCG	2280
TTGGCCGATT CATTAATGCA GCTGGCACGA CAGTTTCCC GACTGGAAAG CGGGCAGTGA	2340
GCGCAACGCA ATTAATGTAA GTTAGCGCGA ATTGTGACCC AAAGCGGCCA TCGTGCCTCC	2400
CCACTCCTGC AGTCGGGGG CATGGATGCG CGGATAGCCG CTGCTGGTTT CCTGGATGCC	2460
GACGGATTTG CACTGCCGGT AGAACTCCGC GAGGTCGTCC AGCCTCAGGC AGCAGCTGAA	2520
CCAACTCGCG AGGGGATCGA GCCCGGGGTG GGCGAAGAAC TCCAGCATGA GATCCCCGCG	2580
CTGGAGGATC ATCCAGCCGG CGTCCCGGAA AACGATTCCG AAGCCCAACC TTTCATAGAA	2640
GGCGCGGGTG GAATCGAAAT CTCGTGATGG CAGGTTGGC GTCGCTTGGT CGGTCATTTC	2700
GAACCCCAGA GTCCCGCTCA GAAGAACTCG TCAAGAAGGC GATAGAAGGC GATGCGCTGC	2760
GAATCGGGAG CGGCGATACC GTAAAGCACG AGGAAGCGGT CAGCCCATTG GCCGCCAACG	2820
TCTTCAGCAA TATCACGGGT AGCCAACGCT ATGTCCTGAT AGCGGTCCGC CACACCCAGC	2880
CGGCCACAGT CGATGAATCC AGAAAAGCGG CCATTTCCA CCATGATATT CGGCAAGCAG	2940
GCATGCCCAT GGGTCACGAC GAGATCCTCG CCGTCGGGCA TGCGCGCCTT GAGCCTGGCG	3000
AACAGTTCGG CTGGCGCGAG CCCCTGATGC TCTTCGTCCA GATCATCCTG ATCGACAAGA	3060
CCGGCTTCCA TCCGAGTACG TGCTCGCTCG ATGCGATGTT TCGCTTGGT GTCGAATGGG	3120
CAGGTAGCCG GATCAAGCGT ATGCAGCCGC CGCATTGCAT CAGCCATGAT GGATACTTTC	3180
TCGGCAGGAG CAAGGTGAGA TGACAGGAGA TCCCTGCCCCG GCACCTCGCC CAATAGCAGC	3240
CAGTCCCTTC CCGCTTCAGT GACAACGTG AGCACAGCTG CGCAAGGAAC GCCCGTCGTG	3300
GCCAGCCACG ATAGCCCGCG TGCCTCGTCC TGCAGTTCAT TCAGGGCACC GGACAGGTG	3360
GTCTTGACAA AAAGAACCGG GCGCCCCCTGC GCTGACAGCC GGAACACGGC GGCATCAGAG	3420
CAGCCGATTG TCTGTTGTGC CCAGTCATAG CGAATAGCC TCTCCACCCA AGCGGCCGG	3480
GAACCTGCGT GCAATCCATC TTGTTCAATC ATGCGAAACG ATCCTCATCC TGTCTCTTGA	3540
TCAGATCTG ATCCCCGTGCG CCATCAGATC CTTGGCGGCA AGAAAGCCAT CCAGTTTACT	3600
TTGCAGGGCT TCCCAACCTT ACCAGAGGGC GCCCCAGCTG GCAATTCCGG TTGCTTGGCT	3660
GTCCATAAAA CCGCCCCAGTC TAGCTATCGC CATGTAAGCC CACTGCAAGC TACCTGCTTT	3720
CTCTTGTGCGC TTGCGTTTTC CCTTGTCCAG ATAGCCAGT AGCTGACATT CATCCGGGGT	3780
CAGCACCGTT TCTGCGGACT GGCTTTCTAC GTGTTCCGCT TCCTTAGCA GCCCTTGCGC	3840
CCTGAGTGCT TGCAGGCAGCG TGAAGCTTAA AAAACTGCAA AAAATAGTTT GACTTGTGAG	3900

CGGATAACAA TTAAGATGTA CCCAATTGTG AGCGGATAAC AATTCACAC ATAAAGAGG	3960
AGAAATTACA TATG	3974

(2) INFORMATION FOR SEQ ID NO:148:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 112 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

AAGCTTAAAA AACTGCAAAA AATAGTTGA CTTGTGAGCG GATAACAATT AAGATGTACC	60
CAATTGTGAG CGGATAACAA TTTCACACAT TAAAGAGGAG AAATTACATA TG	112